

2004-10-32 16:10

us-10-015-480a-180.rni

GenCore version 5.1.6
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leic search, using frame_plus_p2n model

April 9, 2004, 10:40:36 ; Search time 86 Seconds
(without alignments)
1432.548 Million cell updates/sec

US-10-015-480A-180

1189
1 MPKTMHFLFRFVRYLWGL.....HDGDFISPKENVYQHDEL 222

BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

682709 seqs, 277475446 residues

hits satisfying chosen parameters: 1365418

ength: 0

ength: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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n.model DEV=xlh

SP001/US10015480/runat_07042004_080126_28520/app_query.fasta_1.391

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S=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi

GN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

FMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

CGN 1.1.69 @runat_07042004_080126_28520 -NCPD=6 -ICPU=3

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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAEXT=0.5 -FGAPOP=6

OP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

is the number of results predicted by chance to have a

ter than or equal to the score of the result being printed,

ived by analysis of the total score distribution.

SUMMARIES

Query Match	Length	DB ID	Description
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98.9	968	4	US-09-205-258-222
24.9	575	4	US-09-833-381-1564
20.9	570	1	US-07-822-9668-1
20.5	562	5	PCT-US92-03993-6
20.5	2610	2	US-08-989-386-2
16.9	964	4	US-09-023-655-1081
15.7	2157	1	US-08-336-618-25
15.6	450	4	US-09-621-976-2544
15.6	675	1	US-08-707-793A-3
15.6	675	1	US-08-707-792A-3
15.0	571	2	US-08-803-899-1

13	176	14.8	2291	4	US-09-220-132-114	Sequence
14	175	14.7	411	4	US-09-481-620A-84	Sequence
15	174.5	14.7	327	3	US-09-012-515A-34	Sequence
16	174.5	14.7	327	3	US-08-360-144A-34	Sequence
17	174.5	14.7	327	4	US-09-012-504A-34	Sequence
18	174.5	14.7	327	4	US-09-012-399A-34	Sequence
19	174.5	14.7	348	3	US-09-012-515A-5	Sequence
20	174.5	14.7	348	3	US-08-360-144A-5	Sequence
21	174.5	14.7	348	4	US-09-012-504A-5	Sequence
22	174.5	14.7	348	4	US-09-012-399A-5	Sequence
23	174.5	14.7	348	5	PCT-US95-06722-5	Sequence
24	174.5	14.7	690	4	US-09-481-620A-110	Sequence
25	174.5	14.7	1137	1	US-08-707-793A-1	Sequence
26	174.5	14.7	1137	1	US-08-707-792A-1	Sequence
27	174.5	14.7	1155	1	US-08-707-793A-2	Sequence
28	174.5	14.7	1155	1	US-08-707-792A-2	Sequence
29	173	14.6	2246	4	US-09-566-921-48	Sequence
30	172	14.5	443	4	US-09-833-381-1562	Sequence
31	167	14.0	2255	2	US-08-741-134-1	Sequence
32	166.5	14.0	346	4	US-09-621-976-15601	Sequence
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34	166	14.0	357	4	US-09-328-352-1668	Sequence
35	165	13.9	459	4	US-09-833-381-693	Sequence
36	164.5	13.8	879	3	US-08-714-071-3	Sequence
37	163.5	13.8	672	4	US-09-833-381-697	Sequence
38	161.5	13.6	269223	4	US-09-596-002-41	Sequence
39	160	13.5	459	4	US-09-833-381-695	Sequence
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41	152.5	12.8	1236	2	US-08-741-134-5	Sequence
42	144	12.1	417	4	US-09-252-991A-1485	Sequence
43	144	12.1	3591	4	US-09-252-991A-1690	Sequence
44	136.5	11.5	765	4	US-09-489-039A-3743	Sequence
45	136	11.4	1401	4	US-09-252-991A-4911	Sequence

ALIGNMENTS

RESULT 1

US-09-205-258-33

; Sequence 33, Application US/09205258

; Patent No. 6525174

; GENERAL INFORMATION:

; APPLICANT: Young et al.

; TITLE OF INVENTION: 207 Human Secreted Proteins

; FILE REFERENCE: PZ007P1

; CURRENT APPLICATION NUMBER: US/09/205,258

; EARLIER FILING DATE: 1998-12-04

; EARLIER APPLICATION NUMBER: PCT/US98/11422

; EARLIER FILING DATE: 1998-06-04

; EARLIER APPLICATION NUMBER: 60/048,885

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,375

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,881

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,880

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,896

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,020

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,876

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,895

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,884

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,894

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,971

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,964

; EARLIER FILING DATE: 1997-06-06

ICATION NUMBER: 60/048,882
NG DATE: 1997-06-06
ICATION NUMBER: 60/048,899
NG DATE: 1997-06-06
ICATION NUMBER: 60/048,893
NG DATE: 1997-06-06
ICATION NUMBER: 60/048,900
NG DATE: 1997-06-06
ICATION NUMBER: 60/048,901
NG DATE: 1997-06-06
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ICATION NUMBER: 60/048,897
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ICATION NUMBER: 60/048,898
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ICATION NUMBER: 60/048,877
NG DATE: 1997-06-06
ICATION NUMBER: 60/048,878
NG DATE: 1997-06-06
ICATION NUMBER: 60/070,923
NG DATE: 1997-12-18
ICATION NUMBER: 60/092,921
NG DATE: 1998-07-15
ICATION NUMBER: 60/094,657
NG DATE: 1998-07-30
Q ID NOS: 1227
tentIn Ver. 2.0

homo sapiens

ITE
(957)
INATION: n equals a,t,g, or c
ITE
(964)
INATION: n equals a,t,g, or c
33

35: 4.44e-143 Length:
1189.00 Matches:

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-015-480A-180 (1-222) x US-09-205-258-33 (1-971)
QY 1 MetProLysThrMetHisPheLeuPheArgPheHeileValPhePheTyrLeuT:
DB 79 ATGCCAAAACCAATGCAATTTCTTATTCAGATTCATTTCTTTCTTTCTG:
QY 21 PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleG:
DB 139 TTTACTGCTCAGAGACAAAAGAAAGAGAGAGACCCGAGAGAGTGAATAAG:
QY 41 HisArgProGluAenCysSerLysThrSerLysLysGlyAspLeuLeuAenA:
DB 199 CATGCTCCAGAAAACCTGCTCTAAAGACAAAGCAAGAGGAGACCTTACAAATG:
QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnA:
DB 259 GACGGCTACTGGCTAAAGACGGCTCGAAATTTCTACTGACGGCCGACACAA:
QY 81 HisProLysTrpPheValLeuGlyValGlyGlnValLysLysGlyLeuAspI:
DB 319 CACCCCAATGGTTTGTCTTGGTGTGGCAAGTCATATAAAGGCGCTAGACA:
QY 101 ThrAspMetCysProGlyGluLysArgLysValValleProProSerPheA:
DB 379 ACAGATATGTCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATTTG:
QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheG:
DB 439 AAGGAAGCTATGCAAGAGCAAGATTCACCGGATGCTACATTCATTTTGT:
QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleA:
DB 499 CTTTATGCTGTGACCAAGGACACCGAGCATTGAGACATTTAAACAAATAG:
QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluP:
DB 559 AATGACAGGCGCTCTCTAAAGCGGAGATAAACCTCTACTTGCAAGGGAAT:
QY 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIleP:
DB 619 GATGAGAGGCCACGTCACAGTCTATATCAGATGCACTTTTAGAGATATT:
QY 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrG:
DB 679 AATGACCATGATGATGGCTTCATTTCTCCCAAGGATACATGTATACCU:
QY 221 GluLeu 222
DB 739 GAAC TA 744
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US-09-205-258-222
; Sequence 222, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06

ICATION NUMBER: 60/048,880
 NG DATE: 1997-06-06
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 ICATION NUMBER: 60/049,020
 NG DATE: 1997-06-06
 ICATION NUMBER: 60/048,876
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 ICATION NUMBER: 60/048,895
 NG DATE: 1997-06-06
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 NG DATE: 1997-12-18
 ICATION NUMBER: 60/092,921
 NG DATE: 1998-07-15
 ICATION NUMBER: 60/094,657
 NG DATE: 1998-07-30
 ID NOS: 1227

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 ; SEQ ID NO 222
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 ; ORGANISM: Homo sapiens
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 ; NAME/KEY: SITE
 ; LOCATION: (241)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (954)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (961)
 ; OTHER INFORMATION: n equals a,t,g, or c
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 Score: 1176.00 Matches: 222
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 Query Match: 98.91% Indels: 1
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 QY 21 PheThrAlaGlnArgGlnLysGlnGluSerThrGluGluValLysIleGln
 DB 134 TTTACTGCTCAGAGACAAAAGAAAGAGAGAGACCCGAAAGAGTGAATAAG
 QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeu-AsnA
 DB 194 CATGCTCCAGAAACTGCTTAAGCAAGCAAGAAAGAGGAGACCTTAATAATG
 QY 60 rAspGlyTyrluAlaLysAspGlySerLysPheTyrluSerArgThrGlnA
 DB 254 TGACGGCTACCTGGCTAAAGACGGCTCGAAATTCCTACTGACCGCGACACAAA
 QY 80 yHisProLysTrpPheValLeuGlyValGlyGlnValLysGlyLeuAspI
 DB 314 CCACCCCAATGGTTGTTCTTGGTGTGGCAAGTCTATAAAGGCGCTAGACA
 QY 100 tThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheA
 DB 374 GACAGATATGTCCTCGAGAAAGCAAGATTCACCGGATGCTACATGATTTTG
 QY 120 YLysGluGlyTyrlaGluGlyLysIleProProAspAlaThrLeuIlePheG
 DB 434 AAAGGAGGCTATGCAGAAAGCAAGATTCACCGGATGCTACATGATTTTG
 QY 140 uLeuTyrlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleA
 DB 494 ACITTTATGCTGTGACCAAGGACCCGAGCATTTGAGACATTTAAACAAATAG
 QY 160 pAsnAspArgGlnLeuSerLysValaGluIleAsnLeuTyrluGlnArgGluP
 DB 554 CAATGACAGGAGCTCTTAAGCCGAGATMAACCTCTACTTGCAGAGGAAAT
 QY 180 sAspGluLysProArgAspLysSerTyrluAspAlaValLeuGluAspIleP
 DB 614 AGATGAGAGCCACGTCACCAAGTCATATCAGATGCAAGTTTGAAGATATTT
 QY 200 sAsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrluSerValTyrlu
 DB 674 GAATGACCATGATGGTGTGCTTCATTTCTCCCAAGGAATACATGTATACCA

Application PC/TUS9203993
 INVENTION: REKBP: A NOVEL PROLYL ISOMERASE AND
 INVENTION: RAPAMYCIN/FK506 BINDING PROTEIN
 SEQUENCES: 10
 INCE ADDRESS:
 : Hamilton, Brook, Smith & Reynolds, P.C.
 : Two Militia Drive
 : xington
 :A USA
 73
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 PE: Floppy disk
 : IBM PC compatible
 : SYSTEM: PC-DOS/MS-DOS
 : PatentIn Release #1.0, Version #1.25
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 ON NUMBER: PCT/US92/03993
 TE: 19920507
 'ATION:
 CATION DATA:
 ON NUMBER: US 07/697,113
 TE: 08-MAY-1991
 ENT INFORMATION:
 anahan, Patricia
 ION NUMBER: 32,227
 /DOCKET NUMBER: VPI91-05A PCT
 CATION INFORMATION:
 : (617) 861-6240
 : (617) 861-9540
 OR SEQ ID NO: 6:
 ARACTERISTICS:
 562 base pairs
 CLEIC ACID
 ESS: double
 linear
 PE: DNA (genomic)

4.52e-22 Length: 562
 244.00 Matches: 55
 63.25% Conservative: 19
 47.01% Mismatches: 19
 20.52% Indels: 4
 5 Gaps: 3

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 GGGCAAAAGAGAGCTCGACATCGGGGTCAAGAGCGGGTGGACCATGCCCCATCAA 165
 rLysLysGlyAspLeuLeuAsnAlaHisTyrAspGlyTyrLeuAlaLysAspGlySer 69
 GCGCAAGGGGATGCTCTGCATGCTACACAGCGGGAAGCTG--GAAGATGGGACA 222
 sPheTyrCysSerArgThrGluAsnGluGlyHisProLysTrpPheValLeuGlyVal 89
 GTTTGACACAGCGCTGCCCGCAGAACCCAG-----CCCTTTGTCTCTCCCTTTGGCACA 276
 VGLNValIleLysGlyLeuAspIleAlaMetThrAspMetCysProGlyGluLysArg 109
 CCAGGTTCATCAGGGGTGGGACAGGGGTGCTGGGGATGCTGTGAGGGGGAAGCGC 336
 sValValIleProProSerPheAlaTyrGlyLysGluGlyTyrAlaGluGlyLysIle 129
 GCTGGTGTATCCCATCCGAGCTAGGGTATGGAGAGCGGGA---GCTCCCCCAAGATT 393

QY 130 ProProAspAlaThrLeuIlePheGluIleGluLeuTyrAlaValThrLys 1
 Db 394 CCAGGCGGTGCAACCCCTGGTGTTCGAGGTGGAGCTGCTCAAAATAGAGCA 4
 RESULT 6
 US-08-989-386-2
 ; Sequence 2, Application US/08989386
 ; Patent No. 5989860
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: HUMAN ISOMERASE HOMOLOGS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/989,386
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0443 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2610 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: OVARUT01
 ; CLONE: 2255114
 ; US-08-989-386-2
 Alignment Scores:
 Pred. No.: 5.22e-21 Length: 2610
 Score: 243.50 Matches: 65
 Percent Similarity: 52.61% Conservative: 46
 Best Local Similarity: 30.81% Mismatches: 69
 Query Match: 20.48% Indels: 31
 DB: 2 Gaps: 10
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 Db 1186 GTGGAATCAGGACACTGTCCCGCCCATCTGAGACCTGCAATGAGACCCCAAG
 QY 54 AspLeuLeuAsnAlaHisTyrAspGlyTyrLeuAlaLysAspGlySerLysPhe
 Db 1246 GACTTTGTCGATACCAATTACAACTGTCTTCTGTG---GACGGCACCAGCTG
 QY 74 SerArgThrGlnAsnGluGlyHisProLysTrpPheValLeuGlyValGln

[illegible]

081
07879

, Application US/09023655

RATION:

Cocks, Benjamin G.
Susan G. Stuart
Jeffrey J. Sellhamer
VENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENETIC
SEQUENCES: 1508
ENCE ADDRESS:
3: INCYTE PHARMACEUTICALS, INC.
3174 PORTER DRIVE
ALO ALTO
CALIFORNIA
USA
304

3ADABLE FORM:
TYPE: Floppy disk
E: IBM PC compatible
3 SYSTEM: PC-DOS/MS-DOS
: Word Perfect 6.1 for Windows/MS-DOS 6.2

LICATION DATA:
ION NUMBER: US/09/023,655
ATE: HEREWITH
ICATION DATA:
ION NUMBER:
ATE:
CATION:
GENT INFORMATION:
eller, Karen J.
TION NUMBER: 37,071
EDOCKET NUMBER: PA-0001 US
ICATION INFORMATION:
3: (650) 855-0555
(650) 845-4166

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; INFORMATION FOR SEQ ID NO: 1081:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 964 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;     LIBRARY: GENEANK
;     CLONE: g1e2625
;   US-09-023-655-1081

Alignment Scores:
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Score:          200.50      Matches:      60
Percent Similarity: 45.10%      Conservative: 32
Best Local Similarity: 29.41%      Mismatches: 51
Query Match:      16.86%      Indels:      61
DB:              4          Gaps:      7

US-10-015-480A-180 (1-222) x US-09-023-655-1081 (1-964)

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      |||||

QY      40  LeuHis
      ::
Db      279  AAAAATGTGAAGCTTAATGAAGATAAACCCCAAGAAACCAAGTCTGAAGAGAC
      ::|||

QY      47  -----ArgProGluAsnCys-----
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Db      339  GAGGGTCCACAAAATATATACTAAATCTGTCTGAAAAGGGGAGATAAACCAA
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QY      51  LysLysGlyAspLeuLeuAsnAlaHisTyrAspGlyTyrLeuAlaLysAspG1
      |||||
Db      399  AAAAAGGAGATGTTGTTCACTGCTGCTATACAGGACACTA---CAAGATGG
      |||||

QY      71  Phe-----TyrCysSerArgThrGlnAsnGluGlyHisProLY
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Db      456  TTTGATACTAATATTCAAACAAAGTGCACAAAGAAAGAAAATGCCAAGCCTTT
      |||||

QY      86  ValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMetThrAspMe
      ::|||
Db      516  AAGTCGGAGTAGGCAAAAGTTATCAGAGGATGGATCAAGCTCTCTTTGACTAT
      |||||

QY      106  GlyGluLysArgLysValValIleProProSerPheAlaTyrGlyLysGluG1
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Db      576  GGAGAAAGGCTCGACTGGAGATTGAACCAAGATGGCTTACGGAAGAAGAARG
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QY      126  GluglyLysIleProProAspAlaThrLeuIlePheGluIleGluLeuTyrAl
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Db      636  GATGCCAAAATTCACCAAAATGCAAAACACACATTTTGAAGTGAATTA-----
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QY      146  LysGlyProArgSerIleGluThrPheLysGlnIleAspMetAspAsnAspAr
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Db      684  -----GTGGATATTGATTGAAATAG
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QY      166  SerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLysAspGluLY
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Db      711  TTCAGCTCT-----AAGGATATTAG
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QY      186  AspLysSerTyr 189
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Db      738  GATAAAACTTGG 749

RESULT 8
US-08-336-618-25
; Sequence 25, Application US/08336618
; Patent No. 5763590
; GENERAL INFORMATION:
;   APPLICANT: Peattie, Debra A.
;   APPLICANT: Harding, Matthew W.
;   APPLICANT: Livingston, David J.

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ysValVallleProProSerPheAlaTyRGlyysGluGlyTyRAlaGluGlyLysIle 129
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A-CTGTGTATCCCATCCGAGCTAGGTATGGAGCGGGGA--GCTCCCCCAAGATT 356
|||||
roProAspAlaThrLeuIlePheGluIleGluLeuTyRAlaValThrLys 146
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CAGGCGGTGCAACCTG-GTGTTGAGGTGAGCTGCTCAAAATAGAGCGA 406
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3
Application US/08707793A
76696
RMATION:
SALOWE, SCOTT P.
VENTION: A HIGH THROUGHPUT ASSAY USING
SEQUENCES: 17
ENCE ADDRESS:
E: Merck & Co., Inc.
P.O. Box 2000, 126 E. Lincoln Ave.
away
NJ
USA
065-0900
EADABLE FORM:
YPE: Diskette
: IBM Compatible
3 SYSTEM: DOS
: FastSeq for Windows Version 2.0
PLICATION DATA:
ION NUMBER: US/08/707,793A
ATE: 04-SEP-1996
ICATION DATA:
ATION NUMBER:
ATE:
ENT INFORMATION:
amara, Valerie J
TION NUMBER: 35,090
3/DOCKET NUMBER: 19494
ICATION INFORMATION:
3: 908-594-3902
908-594-4720
FOR SEQ ID NO: 3:
CHARACTERISTICS:
675 base pairs
nucleic acid
NESS: single
: linear
YPE: Genomic DNA
3
3:
Length: 675
Matches: 66
ity: 50.00%
Conservative: 33
Mismatch: 33
Indels: 26
Gaps: 11
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TCAGGTGGAACCATC---TCCCGAGGAGATGGACGACCTTCCCGCAAGCGCGCCAG 63
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euLeuAsnAlaHisTyRAspGlyTyRLeuAlaLysAspGlySerLysPheTyRysSer 74
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QY 95 GlyLeuAspIleAlaMetThrAspMetCysProGlyGluLysArgLysValVa
Db 175 GGCTGGGAAGAAGGGGTTGCCAGATGAGTGTGGGTCCAGAGAGCCAACTGAC
QY 115 ProSerPheAlaTyRGlyLysGluGlyTyRAlaGluGlyLysIleProProAs
Db 235 CCAGATTATGCTATGTTGCTGCTGAGGAC---CCAGGCATCATCCACCACA
QY 135 LeuIlePheGluIleGluLeuTyR-----AlaValThrLysGly--
Db 292 CTCGTTCTCGATGTGGAGCTTCTAAACCTGGAGGTCTGTTCCGCGTGGATC
QY 149 ArgSerIleGluThr-----PheLysGlnIleAsp---MetAspAs
Db 352 AACAGCCTGGAGCCCGAACCTGTTCTTCAAGAACCTGAGCGCGCAAGGACGC
QY 164 GlnLeuSerLysAlaGluIleAsnLeu-----TyrLeuGlnArgGluPh
Db 412 CAGCTC---CTGGCGCCCGGGAACACTACGCGCTCCTCTCTCATCCGGGAGAG
QY 181 AspGluLysProArgAspLysSerTyrGlnAsp-----Al
Db 469 ACCGCGGGATCGTTTTCACCTGTCGTCGGGACTTCACAGACAGGAGAGA
QY 195 GluAspIlePheLysLysAsnAspHisAspGlyAspGlyPheIleSerProLy
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RESULT 11
US-08-707-792A-3
; Sequence 3, Application US/08707792A
; Patent No. 5783398
; GENERAL INFORMATION:
; APPLICANT: MARCY, ALICE
; APPLICANT: SALOWE, SCOTT P.
; APPLICANT: WISNIEWSKI, DOUGLAS
; TITLE OF INVENTION: A HIGH THROUGHPUT ASSAY USING
; TITLE OF INVENTION: FUSION PROTEINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/707,792A
; FILING DATE: 04-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Camara, Valerie J
; REGISTRATION NUMBER: 35,090
; REFERENCE/DOCKET NUMBER: 19524
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3902
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

APPLICATION NUMBER: 60/012,054
 FILING DATE: 02/22/1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/087,899
 FILING DATE: 02/21/1997
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: STEFFEN, ERIC K

REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 0609,4240001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600

INFORMATION FOR SEQ ID NO: 1:
 LENGTH: 571 base pairs
 SEQUENCE CHARACTERISTICS:

STRAINEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: CDS
LOCATION: 1..324
803-899-1

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Local Similarity:	30.02%	Miscellaneous:	20

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	2	Gaps:	3
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88 ACCCTG---GACGATGGCCACCAAGTTCGATTCGCGGCAGCGCAACAAAG---

83 LysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMet
139 TTCAAGTTCAACATCGGCAAGGGGAGGTCATCCGTGGCTGGGATGAGGAGT

103 metcysflogigunlysgaryvalvafrroferosefealvayg
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114, Application US/09220132
ent No. 6506607
GENERAL INFORMATION:

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/ NUMBER OF SEQ ID NOS: 132
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 84
/ LENGTH: 411
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: pCANTAB-AP--FKBP--
/ NAME/KEY: misc.structure
/ LOCATION: (1)..(411)
US-09-481-620A-84

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Alignment Scores.

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SCORE:	175 00	Matches:	47

Percent Similarity: 51.08%
Conservative: 24

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Query Match:      14.72%
DBs:              4
Similarity:       14.72%
Indels:           14
Gaps:             5

US-10-015-480A-180 (1-222) x US-09-481-620A-84 (1-411)

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QY || :: || || || ||
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LD CCAAGGAGACGGGGCGCACCTTCCCAAGCAGCGGCAGHACCIGCGTGGTGCACTA

QY 63 T Y L L E A A L A L Y S A S P G L Y S E R L Y S P H E T Y C Y S S E R A R G I N R G I N A S H G L U G I
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... ..
... ..

DB
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Qy 83 LysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMe

205 TTTAAGTTATGCTAGGCAAGCAGGAGTGATCCGAGGCTGGGAAGAGGGGT
Db

103 MetCysProGlyGluLysArgLysValValIleProProSerPheAlaTyrGI
QY

265 ATGAGTGGT CAGAGAGCCAACTGACTATATCTCCAGATTATGCCCTATGG

QY 123 GlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu

db 325 GGGCAC--CCAGGCATCATCCACCATGCCACTCTCGTCTTCGATGTGGA

RESULT 15

US-09-012-515A-34
: Sequence 34. Application US/09012515A

Patent No. 6127521
GENERAL INFORMATION.

APPLICANT: Berlin, Vivian

APPLICANT: Cottarel, Guillaume

; TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS

CORRESPONDENCE ADDRESS:

STREET: One Post Office Square

CITY: BOSTON
STATE: MA

COUNTRY: USA
ZIP: 02109-2170

;;
COMPUTER READABLE FORM:
MEDIUM TYPE: E] comp. disk

COMPUTER: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.30

PLICATION DATA:
ION NUMBER: US/09/012,515A
DATE:

CATION:
ICATION DATA:
ION NUMBER: US 08/360,144
ATE: 20-DEC-1994
GENT INFORMATION:
incient, Matthew P.
ION NUMBER: 36,709
E/DOCKET NUMBER: APV-036.02
ICATION INFORMATION:
E: 617-832-1000
617-832-7000

FOR SEQ ID NO: 34:

HARACTERISTICS:

327 base pairs

ucleic acid

NESS: single

: linear

YPE: DNA

34

S: Length: 327
 Matches: 42
ity: 174.50
 Conservative: 21
larity: 58.88%
 Mismatches: 39
 Indels: 5
 Gaps: 4

180 (1-222) x US-09-012-515A-34 (1-327)

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rgThrGlnAsnGluGlyHisProLysTrpPheValLeuGlyValGlyGlnValIleLys 94
|||     |||     |||     |||     |||     |||     |||     |||     |||
GTGACCGTAAACAG-----CCCTTTAGTTTATGCTAGGCAAGCAGGAGGTGATCCGA 174
lyLeuAspIleAlaMetThrAspMetCysProGlyGluLysArgLysValValIlePro 114
|||     |||     |||     |||     |||     |||     |||     |||     |||
GCTGGGAGAGAGGGGTGCCCCAGATGAGTGTGGTTCAGCGTCCCAACTGACTATATCT 234
roSerPheAlaTyrGlyLysGluGlyTyrAlaGluGlyLysIleProProAspAlaThr 134
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JAGATTATGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 291
auIlePheGluIleGluLeu 141
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TCGCTTCGATGTGGAGCTT 312

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4: April 9, 2004, 12:51:29

3cs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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April 9, 2004, 08:23:49 ; Search time 99 Seconds
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US-10-015-480A-179

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IDENTITY NUC

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682709 seqs, 277475446 residues

hits satisfying chosen parameters: 1365418

length: 0

length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Issued Patents NA:*

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/pCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

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96.7	971	4	US-09-205-258-33	Sequence 33, Appl
95.0	968	4	US-09-205-258-222	Sequence 222, Appl
10.8	575	4	US-09-833-381-1564	Sequence 1564, Ap
7.3	5173	1	US-08-242-677-1	Sequence 1, Appli
7.2	10660	2	US-08-267-803B-8	Sequence 8, Appli
7.2	10660	3	US-09-041-886-16	Sequence 16, Appl
6.9	1129	4	US-09-227-357-40	Sequence 40, Appl
6.9	3994	4	US-09-738-946-7	Sequence 7, Appli
6.7	7724	4	US-08-486-049-1	Sequence 1, Appli
6.7	1776	3	US-08-635-352-10	Sequence 10, Appl
6.7	1776	4	US-09-258-016-10	Sequence 10, Appl
6.7	1776	4	US-09-257-825B-10	Sequence 10, Appl
6.7	964	4	US-09-023-655-1081	Sequence 1081, Ap
6.6	2205	3	US-08-888-077A-41	Sequence 41, Appl
6.6	2058	2	US-08-749-391-1	Sequence 1, Appli
6.6	2058	3	US-09-390-200-1	Sequence 1, Appli
6.6	3200	1	US-08-444-405-1	Sequence 1, Appli
6.6	3200	1	US-08-384-850-1	Sequence 1, Appli
6.6	972	4	US-09-549-831-5	Sequence 5, Appli
6.6	2381	1	US-08-021-608D-9	Sequence 9, Appli
6.6	2381	1	US-08-726-160-9	Sequence 9, Appli
6.6	2381	5	PCT-US94-01782-9	Sequence 9, Appli
6.6	2384	1	US-08-021-608D-1	Sequence 1, Appli
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6.6	2384	5	PCT-US94-01782-1	Sequence 1, Appli
6.5	1357	4	US-09-461-325-55	Sequence 55, Appl
6.5	1357	4	US-10-012-542-55	Sequence 55, Appl

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30	58.6	6.5	1618	4	US-09-800-729-29	Sequenc
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45	58	5.4	2438	4	US-09-393-634-4	Sequenc

ALIGNMENTS

RESULT 1

US-09-205-258-33

; Sequence 33, Application US/09205258

; Patent No. 6525174

; GENERAL INFORMATION:

; APPLICANT: Young et al.

; TITLE OF INVENTION: 207 Human Secreted Proteins

; FILE REFERENCE: P2007P1

; CURRENT APPLICATION NUMBER: US/09/205,258

; CURRENT FILING DATE: 1998-12-04

; EARLIER APPLICATION NUMBER: PCT/US98/11422

; EARLIER FILING DATE: 1998-06-04

; EARLIER APPLICATION NUMBER: 60/048,885

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,375

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,881

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,880

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,896

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,020

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,876

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,895

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,884

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,894

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,971

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,964

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,882

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,899

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; EARLIER APPLICATION NUMBER: 60/048,893

; EARLIER FILING DATE: 1997-06-06

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; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,892

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,915

; EARLIER FILING DATE: 1997-06-06

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 IG DATE: 1997-06-06
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 IG DATE: 1997-12-18
 ICATION NUMBER: 60/092,921
 IG DATE: 1998-07-15
 ICATION NUMBER: 60/094,657
 IG DATE: 1998-07-30
 ID NOS: 1227
 entIn Ver. 2.0

mo sapiens

TE

; LOCATION: (241)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (954)
 ; OTHER INFORMATION: n equals a,t,g, or c
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 ; NAME/KEY: SITE
 ; LOCATION: (961)
 ; OTHER INFORMATION: n equals a,t,g, or c
 US-09-205-258-222

Query Match 95.0%; Score 861.6; DB 4; Length 968;
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 Matches 872; Conservative 4; Mismatches 3; Indels 1;

QY	1	GAGCAGTGTTCGCTGGAGCCGATGCCAAAAACCATGCATTTCTTATTTCAGAT
Db	52	GAGCAGTGTTCGCTGGAGCCGATGCCAAAAACCATGCATTTCTTATTTCAGAT
QY	61	TTTCTTTTATCTGTGGGGCCCTTTTCTCTCAGAGACAAAGAAAGAGGAGA
Db	112	TTTCTTTTATCTGTGGGGCCCTTTTCTCTCAGAGACAAAGAAAGAGGAGA
QY	121	AGAGTGAAATAGAAAGTTTTCATCGTCCAGAAAACCTGCTCTAAGACAAGCA
Db	172	AGAGTGAAATAGAAAGTTTTCATCGTCCAGAAAACCTGCTCTAAGACAAGCA
QY	181	AGACCTACT- AAATGCCATTTATGAGCGCTACTGGCTTAAAGACGGCTCGAAA
Db	232	AGACCTACTNAAATGCCATTTATGAGCGCTACTGGCTTAAAGACGGCTCGAAA
QY	240	GCAGCCGGACACAAATGAAGGCCACCCCAATGTTGTTCTTCTGGTGTGGG
Db	292	GCAGCCGGACACAAATGAAGGCCACCCCAATGTTGTTCTTCTGGTGTGGG
QY	300	TAAAGGGCTAGACATTCATGACAGATATGTGCCCTGGAGAAAAGCGAAAA
Db	352	TAAAGGGCTAGACATTCATGACAGATATGTGCCCTGGAGAAAAGCGAAAA
QY	360	TACCCCTTCATTTGCATACGGAAGGAGGCTATGCAGAGGCAAGATTCCA
Db	412	TACCCCTTCATTTGCATACGGAAGGAGGCTATGCAGAGGCAAGATTCCA
QY	420	CTACATTCATTTTGCAGATTGAACTTTATGCTGTGACCAAGGACCGAGC
Db	472	CTACATTCATTTTGCAGATTGAACTTTATGCTGTGACCAAGGACCGAGC
QY	480	CATTTAAACAAATAGACATGGACATGACAGGAGCTCTCTAAAGCCGAGATA
Db	532	CATTTAAACAAATAGACATGGACATGACAGGAGCTCTCTAAAGCCGAGATA
QY	540	ACTTGCAAGGGAAATTTGAAAAAGATGAGAGCCACGTCGACAAAGTCATATCAG
Db	592	ACTTGCAAGGGAAATTTGAAAAAGATGAGAGCCACGTCGACAAAGTCATATCAG
QY	600	TTTTAGAGATATTTTAAAGAGATGACCATGATGGTGTGCTTCTTCTTCT
Db	652	TTTTAGAGATATTTTAAAGAGATGACCATGATGGTGTGCTTCTTCTTCT
QY	660	AATCAATGTATACCAACACGATGAACTATAGCATATTTGTATTTCTACTTTT
Db	712	AATCAATGTATACCAACACGATGAACTATAGCATATTTGTATTTCTACTTTT
QY	720	AGCTATTTCTGTACTTTTGTATAAAACAAAGTCACATTTTCTCAAGTTGTAT
Db	772	AGCTATTTCTGTACTTTTGTATAAAACAAAGTCACATTTTCTCAAGTTGTAT
QY	780	TTTTTCCCTATGAGAGATATTTTGTATCTCCCAATACATTTGTTGTTAT
Db	832	TTTTTCCCTATGAGAGATATTTTGTATCTCCCAATACATTTGTTGTTAT
QY	840	GTGAGGCTGTTTTGCAAACTTAAAAAAGGCTTTTTTCTCCMAGTTGKAI

879

|||||
 TGAGGCTGTTTGCACAACTTAAAAAATTTAAAAAAA 931

564
 Application US/09833381
 72186
 MATION:
 obison, Keith E.
 ENTION: No. 6672186el Nucleic Acid and Protein Homologs
 CE: 5900-119
 ICATION NUMBER: US/09/833,381
 NG DATE: 2001-04-11
 ATION NUMBER: 09/516,448
 DATE: 2000-02-29
 Q ID NOS: 2050
 stSEQ for Windows Version 3.0
 4

omc sapiens

564
 10.8%; Score 97.6; DB 4; Length 575;
 milarity 59.3%; Pred. No. 6.8e-13;
 Conservative 0; Mismatches 114; Indels 0; Gaps 0;
 3AAGTGAAATAGAGTTTGGCATCGTCAGAAAAGTCTTAAGACAGCAAGAGGG 180
 |||||
 3AAGTGAAATAGAGTTTGGCATCGTCAGAAAAGTCTTAAGACAGCAAGAGGG 322
 |||||
 3ACCTACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTTACTG 240
 |||||
 3ATTTGATGTTGGTCCACTAGAGCTACTTAGAAAAGAGCGCTCTTATTTCACTC 382
 |||||
 AGCCGACACAAATGAGGCGCACCCCAATGGTTTGTGTTGGTGGGCAAGTCAT 300
 |||||
 ACTCAACACATACAAATGTCAGGCCATTGTTGTTTACCTGGGCATCTCGAGGCTCT 442
 |||||
 AAGGCTAGACATTGCTATGACATATGTCCTCGGAGAAAGCGAAAGTACTTAT 360
 |||||
 AAGGTTGGACACAGGCTTGAAGGAATGTTGTAGGAGAGAGAAAGTCATCAT 502
 |||||
 CCCCCTTATTTGCATACGGAAGGAGGCTATGCAGAA 400
 |||||
 CTTCTGCTGCTGGCTATGGAAGAGGAGGAAAGGTAA 542
 |||||

pplication US/08242677
 77143
 MATION:
 Gaynor, Richard B
 Wu, Foon W.
 VENTION: Cellular Nucleic Acid Binding Protein
 VENTION: and Uses thereof in regulating Gene Expression and in the
 VENTION: Treatment of AIDS
 SEQUENCES: 9
 ZNCE ADDRESS:
 S: Arnold, White & Durkee
 P.O. Box 4433
 ouston
 TX
 USA
 210
 SADBABLE FORM:
 YPE: Floppy disk
 : IBM PC compatible
 3 SYSTEM: PC-DOS/MS-DOS
 : PatentIn Release #1.0, Version #1.25
 PLICATION DATA:

APPLICATION NUMBER: US/08/242,677
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mayfield, Denise L.
 REGISTRATION NUMBER: 33,732
 REFERENCE/DOCKET NUMBER: UTSD:401
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 713-787-1400
 TELEFAX: 713-789-2679
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5173 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..4863
 US-08-242-677-1

Query Match 7.3%; Score 65.8; DB 1; Length 5173;
 Best Local Similarity 61.0%; Pred. No. 1.3e-05;
 Matches 125; Conservative 0; Mismatches 77; Indels 3;
 QY 703 TTCTACTTTTTTTTGTAGCTATTTACTGTTACTTATGTATATGTAATAAACAGAGTCA
 |||||
 Db 4952 TTGTGTAATTTGTAATTTCTTTTCTTGTCAATTTAATGCCAAAGTTTGCCCA
 |||||
 QY 763 CCAAGTGTGTAATTTGCTATTTTCCCTCATGAGAAGATATTTTGATCTCCCCAA
 |||||
 Db 5012 TAAACATATTTACTATATATTTTCCCTTTTAAATAACACTTTTGT---TAAAT
 |||||
 QY 823 ATTTGGTATAATAATGTGAGGCTGTTTGGCAACTTAAAAA
 |||||
 Db 5069 TTCCTTTAAATAAATATTTTAAAGCAATTTGTCCAATAAAAAA
 |||||
 QY 883 AAAAAA
 |||||
 Db 5129 AAAAAA
 |||||

RESULT 5
 US-08-267-803B-8
 ; Sequence 8, Application US/08267803B
 ; Patent No. 5834183
 ; GENERAL INFORMATION:
 ; APPLICANT: Orr, Harry T.
 ; APPLICANT: Ranum, Laura P.W.
 ; APPLICANT: Chung, Ming-Yi
 ; APPLICANT: Zoghbi, Huda Y.
 ; TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
 ; Patent No. 5834183
 ; TITLE OF INVENTION: Type 1 and Method for Diagnosis
 ; NUMBER OF SEQUENCES: 85
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Mueiting, Raasch, Gebhardt & Schwappach, P.A.
 ; STREET: P.O. Box 581415
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55458-1415
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/267,803B
 ; FILING DATE: 28-JUN-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:

Cormack, Myra H.
 PION NUMBER: 36,602
 3/DOCKET NUMBER: 110.00030120
 CATION INFORMATION:
 3: 612-305-1217
 612-305-1228
 FOR SEQ ID NO: 8:
 CHARACTERISTICS:
 10660 base pairs
 acleic acid
 ESS: single
 : linear
 ?PE: DNA

CDS
 936..3384

7.2%; Score 65.2; DB 2; Length 10660;
 ilarity 58.9%; Pred. No. 2.2e-05;
 Conservative 0; Mismatches 78; Indels 0; Gaps 0;
 AGTATTACTGACATTATGTATATAAAACAAAGTCACCTTTCTCCAAAGTTGTATTCG 777
 ATTTCATTATATAATAAAACAATGTTGATTCAAAATTTGAACAAAATTTGTTTAAA 10530
 TTTTCCCTATGAGAGATATTTTGATCTCCCAATACATGATTTGCTATAATAA 837
 AATGCTGTATACCAAGTACAGTTTATGTTTCAGTATACCTGCTACTATAATAA 10590
 GTGAGGCTGTTTGCACAACTTAAACAAAAAATAAATAAATAAATAAATAAATAA 897
 GTGCCAATTCGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 10650

AAAAAAA 907
 |||||
 AAAAAAA 10660

pplication US/09041886
 5872

MATION:
 Bredeesen, Dale E.
 Rabizadeh, Sharoz
 VENTION: Proapoptotic Peptides, Dependence
 VENTION: Polypeptides and Methods of Use
 EQUENCES: 72

NCE ADDRESS:
 : Campbell & Flores LLP
 4370 La Jolla Village Drive, Suite 700
 n Diego
 alifornia
 United States
 22

ADABLE FORM:
 PE: Floppy disk
 IBM PC compatible
 SYSTEM: PC-DOS/MS-DOS
 Patent in Release #1.0, Version #1.25
 LICATION DATA:
 ON NUMBER: US/09/041,886
 TE:

ATION:
 ENT INFORMATION:
 mpbell, Cathryn A.
 ION NUMBER: 31,815
 /DOCKET NUMBER: P-LJ 2626
 CATION INFORMATION:
 : (619) 535-9001
 (619) 535-8949
 OR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
 LENGTH: 10660 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 936..3384
 US-09-041-886-16

Query Match 7.2%; Score 65.2; DB 3; Length 10660;
 Best Local Similarity 58.9%; Pred. No. 2.2e-05;
 Matches 112; Conservative 0; Mismatches 78; Indels 0;

QY 718 TTAGCTATTACTGTACTTTATGTATATAAAACAAAGTCACCTTTCTCCAAAGTTG
 DB 10471 TTAATTCATTATTAATAATAAAACAATGTTGATTCAAAATTTGAACAAAATTTG
 QY 778 TATTTTCCCTATGAGAGATATTTTGATCTCCCAATACATGATTTGCT
 DB 10531 TAAATGCTGTATACCAAGTACAAAGTTTATGTTTTCAGTATACTCGTACTAAT
 QY 838 ATGTGAGGCTGTTTGCACAACTTAAACAAAAAATAAATAAATAAATAAATAA
 DB 10591 CAGTCCCAATTCGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA
 QY 898 AAAAAAAA 907
 DB 10651 AAAAAAAA 10660

RESULT 7

US-09-227-357-40
 ; Sequence 40, Application US/09227357
 ; Patent No. 6342581
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischer et al.
 ; TITLE OF INVENTION: 123 Human Secreted Proteins
 ; FILE REFERENCE: PZ010F1
 ; CURRENT APPLICATION NUMBER: US/09/227,357
 ; CURRENT FILING DATE: 1999-01-08
 ; EARLIER APPLICATION NUMBER: PCT/US98/13684
 ; EARLIER FILING DATE: 1998-07-07
 ; EARLIER APPLICATION NUMBER: 60/051,926
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,793
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,925
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,929
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,803
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,732
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,931
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,932
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,916
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,930
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,918
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,920
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,733
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/052,795
 ; EARLIER FILING DATE: 1997-07-08
 ; EARLIER APPLICATION NUMBER: 60/051,919

pplication US/09738946
79701
MATION:

APPLICANT: EXELIXIS, INC.
 TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEIN
 FILE REFERENCE: EX00-043C
 CURRENT FILING DATE: 2000-12-14
 PRIOR FILING DATE: 2000-12-14
 PRIOR FILING DATE: 1999-12-14
 PRIOR FILING DATE: 1999-12-14
 PRIOR FILING DATE: 1999-12-14
 PRIOR FILING DATE: 2000-01-28
 PRIOR FILING DATE: 2000-02-29
 PRIOR FILING DATE: 2000-02-29
 PRIOR FILING DATE: 2000-03-01
 PRIOR FILING DATE: 2000-03-15
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 7
 LENGTH: 3994
 TYPE: DNA
 ORGANISM: Drosophila melanogaster
 US-09-738-946-7

Query Match 6.9%; Score 62.6; DB 4; Length 3994;
 Best Local Similarity 73.4%; Pred. No. 6.4e-05;
 Matches 80; Conservative 0; Mismatches 29; Indels 0;

QY 799 TATTTTGATCTCCCAATACATTGATTTTGGTATATAAAATGTGAGGCTGTTT
 Ddb 3263 TAGTTTATTTTCTTAATTTGTTATGTTCTGCAATTAATATGACCTCTTAT

QY 859 TTAAAAA AA 907
 Ddb 3323 AA 337

RESULT 9
 US-08-486-049-1
 Sequence 1, Application US/08486049
 Patent No. 6572862
 GENERAL INFORMATION:
 APPLICANT: Estes, Mary K
 APPLICANT: Jiang, Xi
 APPLICANT: Graham, David Y
 TITLE OF INVENTION: Methods and Reagents to Detect and
 TITLE OF INVENTION: Characterize No. 6572862walk and Related
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fulbright & Jaworski L.L.P.
 STREET: 801 Pennsylvania Ave., N.W.
 CITY: Washington, D.C.
 STATE:
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,049
 FILING DATE: June 7, 1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Davis, Peter
 REGISTRATION NUMBER: 36,119
 REFERENCE/DOCKET NUMBER: 311.023
 TELECOMMUNICATION INFORMATION:

10:32:15 2004

us-10-015-480a-179.rni

202-662-0200
202-662-4643

OR SEQ ID NO: 1:

CHARACTERISTICS:

7724 base pairs

cleic acid

ESS: single

unknown

PE: cDNA

URGE: No. 6572862walk virus

8FIIa

L ISOLATE: 8FIIa

COURCE: UCNV-953 and its derivatives

CDS
146..5359

ORAMATION: /note= "The protein encoded by

ORAMATION: nucleotides 146 through 5359 is eventually cleaved

ORAMATION: to make at least a picornavirus 2c-like protein, a

ORAMATION: 3C-like protease and an RNA-dependent RNA polymerase.

CDS

5346..6935

ORAMATION: /note= "Nucleotides 5346 through

ORAMATION: 5359 are used for coding two different amino acid

ORAMATION: sequences: the first is the sequence coded by

ORAMATION: nucleotides 146 through 5359, the second by nucleotides

ORAMATION: 5346 through 6935.

CDS

6938..7573

ilarity 6.7%; Score 61; DB 4; Length 7724;

Conservative 0; Mismatches 20; Indels 0; Gaps 0;

ACATTGATTGGTATATTAATGTGAGGCTGTTTGGCAACTTAAAAA 874

TCATTAAATTAGGTTTAATTAGGTTTAATTGATGTTAAAAA 7663

AAAAAAAAAAAAAAAAAAAAAAAAAAAA 907

AAAAAAAAAAAAAAAAAAAAAAAAAAAA 7696

plication US/08655352

9991

ATION:

Bachettira W. Poovaiah, Zhihua Liu,

Shameekumar Patil, Daisuke Takezawa

ENTION: COMPOSITIONS AND METHODS FOR

SEQUENCES: 19

ACE ADDRESS:

: Klarquist Sparkman Campbell Leigh &

: Winston, LLP

One World Trade Center

121 S.W. Salmon Street

Suite 1600

Portland

region

United States of America

04

ADABLE FORM:

PE: Disk, 3-1/2 inch

IBM PC compatible

SYSTEM: MS DOS

SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA: US/08/655,352
APPLICATION NUMBER: US/08/655,352
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,449
FILING DATE: October 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-45000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: Tobacco CCaMK cDNA and deduced amino-acid
FEATURE:
NAME/KEY: protein-coding sequence (not including
NAME/KEY: stop codon)
LOCATION: nucleotides 20-1570
US-08-655-352-10
Query Match 6.7%; Score 60.8; DB 3; Length 1776;
Best Local Similarity 54.0%; Pred. No. 0.00013;
Matches 149; Conservative 0; Mismatches 122; Indels 5;
QY 637 TGATGGCTTCATTTCCTCCCAAGGAATACAATGTATATACCAACACGATGAAGTATATA
Db 1498 TGATGAGTTCAGAGCTGCTATGCAAGAGAGATAGTTCCTTCAAGATGATGCTCT
QY 697 TTGATTTTCTACTTTTTTTTTTTAGCTATTACTGT-----ACTTTATGTATAA
Db 1558 TCTTCGCTCCCTCTTAATTAATTCCTTTTAAATTTTGGCTCTCTTTTAAATTTGT
QY 752 GTCACCTTTCTCCCAAGTGTGATTTGCTATTTCCTTCCTATGAGAAGATATTTC
Db 1618 ACGTAATCTATTAATCTCTAATCTCTAATCTCTATGACATGCAATGATTTATTTT
QY 812 CCAATACATTTGATTTGGTATAATAAATGTGAGGCTGTTTTCGAACTTAAAAA
Db 1678 ACTCGTAAAAAGATCCTTTAAATTAATTCGGAAGCCTTTATGTTAAAAA
QY 872 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 907
Db 1738 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1773

RESULT 11

US-09-258-016-10

; Sequence 10, Application US/09258016

; Patent No. 6362395

; GENERAL INFORMATION:

; APPLICANT: Bachettira W. Poovaiah, Zhihua Liu,

; APPLICANT: Shameekumar Patil, Daisuke Takezawa

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klarquist Sparkman Campbell Leigh &

; ADDRESSEE: Winston, LLP

; STREET: One World Trade Center

; STREET: 121 S.W. Salmon Street

; STREET: Suite 1600

; CITY: Portland

; STATE: Oregon

United States of America

204

READABLE FORM:

YFE: Disk, 3-1/2 inch

G SYSTEM: MS DOS

PPLICATION DATA:

ION NUMBER: US/09/258,016

ATE:

CATION:

GENT INFORMATION:

tephens Jr., Donald L.

TION NUMBER: 34,022

E/DOCKET NUMBER: 4630-51994

ICATION INFORMATION:

E: (503) 226-7391

FOR SEQ ID NO: 10:

1776 base pairs

ucleic acid

NESS: double stranded

: linear

YFE: CDNA to mRNA

ION: Tobacco CcAmK cDNA and deduced amino-acid

ION: sequence

: protein-coding sequence (not including

: stop codon)

: nucleotides 20-1570

0

6.7%; Score 60.8; DB 4; Length 1776;

milarity 54.0%; Pred. No. 0.00013;

Conservative 0; Mismatches 122; Indels 5; Gaps 1;

GATGGCTTCATTCTCCCAAGGATACAAATGTATACCAACAGCATGATAGCATAT 696

|||||

GATGAGTTCAAGCTGCTATGCAAGAGATAGTCCCTTCAAGATGAGTCTCTCTTC 1557

|||||

TGATATTCACATTTTCTTTTCTAGCTATTACTGT-----ACTTATGATATAAAACAA 751

|||||

CTTCGCTCCCTCTTAATTAATTCCTTTTATGAAATTTTGGCTCTCTTTAAATTTGTAATAAC 1617

|||||

TCACATTTCTCCAGTGTATTGCTATTTTCCCTCATGAGAAGATATTGATCTCC 811

|||||

CCCTAATCTATTAATCTCTAACTTCTCTGACATGCAATGATTTATTTTATCACT 1677

|||||

CAATACATTTGATTTTGGTATAATAATGTGAGGCTGTTTTCGAACTTAAACAAAAA 871

|||||

CTCGTAAAAAGATCCTTTTAAATTAATTCGGAAGCCTTTATGTTAAACAAAAA 1737

|||||

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 907

|||||

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1773

|||||

10 Application US/09257825B

03352

MATION:

oovaiyah, Bachettira W.

Patil, Shameekumar

Takezawa, Daisuke

ENTION: Compositions and Methods for Production of Male-Sterile Plants

CE: 4630-51993

NG DATE: 1999-02-25

ATION NUMBER: US 08/655,352

DATE: 1996-05-23

INFORMATION FOR SEQ ID NO: 1081:

; PRIOR FILING DATE: 1996-03-28
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 1776
 ; TYPE: DNA
 ; ORGANISM: Nicotiana tabacum
 US-09-257-825B-10

Query Match 6.7%; Score 60.8; DB 4; Length 1776;
 Best Local Similarity 54.0%; Pred. No. 0.00013;
 Matches 149; Conservative 0; Mismatches 122; Indels 5;

QY 637 TGATGGCTTCATTCTCCCAAGGATACAAATGTATACCAACAGCATGAGTAACTAT

Db 1498 TGAAGATTCAAGCTGCTATGCAAGAGATAGTCCCTTCAAGATGTAGTCC

QY 697 TTGTATTTCTACTTTTTTTTTTTTAGCTATTACTGT-----ACTTTATGTATA

Db 1558 TCTTGTGCTCTTAAATTAATTCCTTTATGATTTTGGCTCTTTTAAATTG

QY 752 GTCACATTTCTCCAGTGTATTTGCTATTTTCCCTCATGAGAAGATATTTT

Db 1618 ACCTAAATTCATTAATATATCTTAATCTTCTATGACATGCAATGCAATTTATTTT

QY 812 CCAATACATTTGATTTTGGTATAATAATGAGGCTGTTTTCGAACTTAAAC

Db 1678 ACTCGTAAAAAGATCCTTTAAATTAATTCGGAAGCCTTTTATGTTAAAC

QY 872 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 907

Db 1738 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1773

RESULT 13

US-09-023-655-1081
 ; Sequence 1081, Application US/09023655
 ; Patent No. 6607879
 ; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CE

; TITLE OF INVENTION: EXPRESSION
 ; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO

; STATE: CALIFORNIA
 ; COUNTRY: USA

; ZIP: 94304
 ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/023,655

; FILING DATE: HEREWITH
 ; CLASSIFICATION:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:

; FILING DATE:
 ; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0001 US

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1081:

CHARACTERISTICS:
964 base pairs
cleic acid
ESS: single
linear
SOURCE:
GENBANK
182625
81

6.7%; Score 60.4; DB 4; Length 964;
ilarity 56.6%; Pred. No. 0.00013;
Conservative 0; Mismatches 86; Indels 0; Gaps 0;
CACAAATGAAGCCACCCCAATGCTTTGTTCTTGGTGTGGCAAGTCATATAAGG 306
AGAGAAAATGCCAAGCCTTTAAGTTTAAAGTCGGAGTAGGCAAGATTACAGAGG 544
TAGACATTGCTATGACAGATATGTCCTCGGAGAAAGCGAAAAGTAGTTATACCCCC 366
GGGATGAAGCTCTCTTGAATGATGATGATGATGATGATGATGATGATGATGATG 604
CATTTGCATACGAAGAGGAGGCTATGCGAGAGGCAAGATTCCACCGATGCTACATT 426
AATGGCTTACGGAAAGAGGACAGCTGATGCCAAATTCACCAAAATGCAAAACT 664

TTTTTGAGATTGAAT 444
|||||
CTTTGAAGTGAATT 682

1
Publication US/0888077A
0143

MATION:
ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
VENTION: GENETIC SEQUENCES AND PROTEINS RELATED
VENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
SEQUENCES: 41

NCE ADDRESS:
: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
600 SOUTH AVENUE WEST
STFIELD
J

USA
90-1497
ADABLE FORM:
PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
ASCII
LOCATION DATA:
ON NUMBER: US/08/888,077A
TE: 03-JUL-1997

ATION: 530
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ON NUMBER: US 08/592,541
TE: 26-JAN-1996
ENT INFORMATION:
LISI, THOMAS M

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/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP CIP IV
CATION INFORMATION:
: (908) 654-5000
(908) 654-7866
OR SEQ ID NO: 41:
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TOPOLOGY: linear
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NAME/KEY: misc feature
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Best Local Similarity 64.3%; Pred. No. 0.00019;
Matches 83; Conservative 1; Mismatches 45; Indels 0;
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Db 2034 AGTTGCTCTTTTATAGGAATNTTTTGGAAATTTGGGAGCAGCATGATTGATT
QY 839 TGTGAGGCTGTTTGGAACTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA
Db 2094 TTAAGATNTTTTACACATTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA
QY 899 AAAAAAAA 907
Db 2154 AAAAAAAA 2162

RESULT 15

US-08-749-391-1
; Sequence 1, Application US/08749391
; Patent No. 5948667
; GENERAL INFORMATION:
; APPLICANT: Cheng, Kuo-Joan
; APPLICANT: Selinger, Leonard B.
; APPLICANT: Liu, Jin-Hao
; APPLICANT: Hu, Youji
; APPLICANT: Forsberg, Cecil W.
; APPLICANT: Moloney, Maurice M.
; TITLE OF INVENTION: A Xylanase Obtained From an
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80803
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,391
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Donna M. Ferber
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 93-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2058 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Neocallimastix patriciarum
; STRAIN: 27


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: 301..1755

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d: April 9, 2004, 10:40:29
secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using sw model

April 9, 2004, 08:12:55 ; Search time 3215 Seconds
(without alignments)
8424.572 Million cell updates/sec

US-10-015-480A-179

907
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IDENTITY NUC

Gapop 10.0 , Gapext 1.0

27513289 seqs, 14931090276 residues

hits satisfying chosen parameters: 55026578

length: 0
length: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
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- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

is the number of results predicted by chance to have a
iter than or equal to the score of the result being printed,
tived by analysis of the total score distribution.

SUMMARIES

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72.4	786	14	CF593540		CF593540 AGENCOURT

5	636	70.1	643	12	BG939266	BG939266
6	625.2	68.9	943	14	CD557479	CD557479
7	618.4	68.2	690	14	CA412939	CA412939
8	600	66.2	618	12	BG939267	BG939267
9	585.2	64.5	734	10	BE874396	BE874396
10	536.4	59.1	602	13	EX485892	EX485892
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18	473	52.1	643	14	CF792774	CF792774
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ALIGNMENTS

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LOCUS
DEFINITION Homo sapiens FK506-binding protein mRNA, complete cds.
ACCESSION AF092137
VERSION AF092137.1 GI:5138923
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
1 (bases 1 to 1231)
Han,Z., Song,H., Dai,M., Huang,Q., Mao,Y., Zhang,Q., Ma
Luo,M., Chen,J. and Hu,R.
Huan FK506-binding protein mRNA, complete cds
REFERENCE 2 (bases 1 to 1231)
AUTHORS Han,Z.
TITLE Direct Submission
JOURNAL Submitted (16-SEP-1998) Shanghai Second Medical Univers
Hospital, Shanghai Institute of Hematology, 197 Rui-Jin
Shanghai 200025, P.R. China
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Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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ACCESSION BI827688
VERSION BI827688.1 GI:15939238
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 800)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collectic
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LI
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution informatio
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Date: L14M1412 row: n column: 23
High quality sequence stop: 794.
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/notes="Organ: brain; Vector: pCMV-SPORT6; Site
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directionally cloned (EcoRV site is destroyed
cloning). Average insert size 1.3 kb, insert
0.9-3 kb. Library is normalized and enriched
full-length clones and was constructed by C.
(Invitrogen). Research Genetics tracking cod
this is a NIH_MGC Library."

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Query Match 75.0%; Score 679.8; DB 12; Length 800;
Best Local Similarity 98.8%; Pred. No. 9.4e-79;
Matches 738; Conservative 0; Mismatches 2; Indels 7;
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 COURT_13903492 NIH_MGC_147 Homo sapiens cDNA clone
 S:30341652 5', mRNA sequence.

9909
 9909.1 GI:30284429

sapiens (human)

sapiens
 cyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

bases 1 to 787

MGC http://mgi.nci.nih.gov/
 ional Institutes of Health, Mammalian Gene Collection (MGC)
 ublished (1999)

act: Robert Strausberg, Ph.D.

l: cgapbs-remail.nih.gov

le Procurement: Dr. Stefan Hansson

A Library Preparation: Michael J. Brownstein (NHGRI) with help
 advice from Piero Carninci (RIKEN)

A Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Sequencing by: Agencourt Bioscience Corporation

re distribution: MGC clone distribution information can be

through the I.M.A.G.E. Consortium/LLNL at:

://image.llnl.gov

e: NDAM373 row: h column: 13

quality sequence stop: 621.

Location/Qualifiers

1. .787

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/clone_lib="NIH_MGC_147"

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 primary library enriched for full-length clones
 constructed using the Cap-trapper method (Carri
 preparation). Library constructed by M. Brown
 (NIH/NHGRI, National Institutes of Health). NC
 a NIH_MGC library."

ORIGIN

Query Match 72.9%; Score 661.4; DB 14; Length 787;
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RESULT 4

CF593540

LOCUS

CF593540 786 bp mRNA linear EST

DEFINITION

AGENCOURT_15624003 NIH_MGC_147 Homo sapiens cDNA clone

IMAGE:30531031 5', mRNA sequence.

ACCESSION

CF593540

VERSION

CF593540.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

o sapiens
 aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 malia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 (bases 1 to 786)
 -MGC http://mgi.nci.nih.gov/
 ional Institutes of Health, Mammalian Gene Collection (MGC)
 ublished (1999)
 tact: Daniela S. Gerhard, Ph.D.
 ice of Cancer Genomics
 ional Cancer Institute / NIH
 3. 31 Rm10A07 Bethesda, MD 20892
 il: cgabs-remail.nih.gov
 sue Procurement: Dr. Stefan Hansson
 NA Library Preparation: Michael J. Brownstein (NHGRI) with help
 advice from Piero Carninci (RIKEN)
 NA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 A Sequencing by: Agencourt Bioscience Corporation
 one distribution: MGC clone distribution information can be
 nd through the I.M.A.G.E. Consortium/LNL at:
 p://image.lnl.gov
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 n quality sequence stop: 623.
 Location/Qualifiers
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 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: This is
 a NIH_MGC library."

72.4%; Score 656.8; DB 14; Length 786;
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 Conservative 0; Mismatches 2; Indels 4; Gaps 4;

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 CCCCCTTCATTTGCATACGGAAGGAGGCTATGACAGAGGCAAGATTCACCGGATGC 420
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 CCCCCTTCATTTGCATACGGAAGGAGGCTATGACAGAGGCAAGATTCACCGGATGC 498
 |||||

QY 421 TCAATTGATTTTGGAGATTGAACCTTTATGCTGTGACCAAGGACCAAGGAGCA
 |||||
 Db 499 TCAATTGATTTTGGAGATTGAACCTTTATGCTGTGACCAAGGACCAAGGAGCA
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 QY 481 ATTAAACAAATAGACATGACAAATGACAGGAGGAGCTCTCTAAAGCCGAGATAA
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 Db 559 ATTAAACAAATAGACATGACAAATGACAGGAGGAGCTCTCTAAAGCCGAGATAA
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 QY 541 CTTGCAAGGGAATTTGAAAGAGATGAGAGCCACCTGACCAAGTCTATATCAGG
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 Db 619 CTTGCAAGGGAATTTGAAAGAGATGAGAGCCACCTGACCAAGTCTATATCAGG
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 QY 601 TTTAGAGATA-TTTTAAAGAGATGACCAATGATGATGTA-TGGCTTCATTTC
 |||||
 Db 679 TTTAGAGATA-TTTTAAAGAGATGACCAATGATGATGTA-TGGCTTCATTTC
 |||||
 QY 659 GAATCAATGTATA-CCAAACAGATGAATAG-CATATTTGTATTT 704
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 Db 739 GAATCAATGTATA-CCAAACAGATGAATAG-CATATTTGTATTT 786
 |||||

RESULT 5
 BG939266 643 bp mRNA linear EST
 LOCUS
 cn31e10.x1 Normal Human Trabecular Bone Cells Homo sapi
 clone NHTBC_cn31e10 random, mRNA sequence.
 DEFINITION
 BG939266
 ACCESSION
 BG939266
 VERSION
 BG939266.1 GI:14338638
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Ho
 1 (bases 1 to 643)
 Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,
 Beckstrom-Youngberg,S.M., Green,E.D., Powell,J.I., Yang
 Robey,P.G., Hotchkiss,R.N. and Francomano,C.A.
 SGAP: The Skeletal Genome Anatomy Project
 Unpublished (1997)
 CONTACT: Libin Jia
 Medical Genetics Branch
 National Human Genome Research Institute
 10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267
 Tel: 301-402-4877
 Fax: 301-496-7157
 Email: libin@helix.nih.gov
 DNA Sequencing and analyses by National Institutes of H
 Intramural Sequencing Center (NISC).
 Plate: 31 row: e column: 10
 Seq primer: -21M13 forward primer (ABI).
 Location/Qualifiers
 1. .843
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="NHTBC_cn31e10"
 /sex="Female"
 /tissue_type="Bone"
 /cell_type="Trabecular Bone Cells"
 /lab_host="SURE"
 /clone_lib="Normal Human Trabecular Bone Cells"
 /note="Organ: Hip; Vector: pBluescript; Site 1
 Library constructed by Dr. Marian Young and Dr
 Gehron Robey (NIDCR)"

ORIGIN
 Query Match 70.1%; Score 636; DB 12; Length 643;
 Best Local Similarity 100.0%; Pred. No. 4.8e-73;
 Matches 636; Conservative 0; Mismatches 0; Indels 0;
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 QY 76 GGGCCTTTTACTGCTCAGACAAAGAGAGAGAGACCGAAGAGTGA
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H-EZO-bao-1-19-0-UI 3', mRNA sequence.

112939

112939.1 GI:24775590

no sapiens (human)

no sapiens

aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 690)

(-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>).

ional Cancer Institute, Cancer Genome Anatomy Project (CGAP),

or Gene Index

ublished (1997)

taact: Robert Strausberg, Ph.D.

ail: cgapbs-re@mail.nih.gov

ssue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of

hoapedics

NA library preparation: Dr. M. Bento Soares, University of Iowa

NA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

TA Sequencing by: Dr. M. Bento Soares, University of Iowa

one Distribution: Clone distribution information can be obtained

m Dr. M. Bento Soares, bento-soares@uiowa.edu

(primer: M13 FORWARD

YA-Yes.

Location/Qualifiers

1. .690

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-EZO-bao-1-19-0-UI"

/tissue_type="Chondrosarcoma Grade II"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP Chl"

/note="Organ: Left Pelvis; Vector: p77T3-Pac (Pharmacia)

with a modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI_CGAP_Ch1 is a cDNA library containing the following

tissues): Chondrosarcoma Grade II. The library was

constructed according to Bonaldi, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dT primer containing a

Not I site. Double stranded cDNA was ligated to an EcoR I

adaptor, digested with Not I, and cloned directionally

into p77T3-Pac vector. The oligonucleotide used to prime

the synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the

(dT)18 tail. The sequence tag for this library is

TGATCACGCT

TAG TISSUE=grade-2-chondrosarcoma

TAG_LIB=UI-H-EZO

TAG_SEQ=ATCTAATATG

68.2%; Score 618.4; DB 14; Length 690;

ilarity 98.7%; Pred. No. 8.4e-71;

Conservative 0; Mismatches 3; Indels 6; Gaps 6;

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CTAAATGCCATTATGACGGCTACCTGGCTAAAGCGGCTCG-ATTTACTGCAGCCG 632

ACACAAATGAGGCGACCCCAATGGTTTGTGTTGTTGGGCAAGTCATAAAGG 306

ACACAAATG-AGGCCACCCCAATGG-TTGTTCCTTGTGTTGGGCAAGTCATAAAGG 574

CTAGACATTGCTATGACAGATATGTCCTCGGAGAAAGCGAAAGTAGTTATACCCC 366

CTAGACATTGCTATGACAGATATGTCCTCGGAGAAAGCGAAAGTAGTTATACCCC 514

TCATTTGCATACGGAAGGAGGCTATGACAGAGGCAAGATTCACCGGATGTCATT 426

TCATTTGCATACGGAAGGAGGCTATGACAGAGGCAAGATTCACCGGATGTCATT 454

Qy 427 GATTTTGGAGATTGAACCTTTATGCTGTGACCCAAAGGACCACGGAGCATTGAG

Db 453 GATTTTGGAGATTGAACCTTTATGCTGTGACCCAAAGGACCACGGAGCATTGAG

Qy 487 ACAAATAGACATGACCAATGACAGGCGAGCTCTCTAAAGCCGAGATAAACCTC

Db 393 ACAAATAGACATGACCAATGACAGGCGAGCTCTCTAAAGCCGAGATAAACCTC

Qy 547 AAGGGAATTTGAAAAGACATGAGAACCCAGTGCACAACTCATATCAGGATGCA

Db 333 AAGGGAATTTGAAAAGACATGAGAACCCAGTGCACAACTCATATCAGGATGCA

Qy 607 AGATATTTTAAAGAAAGATGACCATGATGGTGTGATGGTTCATTTCTCCCAAG

Db 273 AGATATTTTAAAGAAAGATGACCATGATGGTGTGATGGTTCATTTCTCCCAAG

Qy 667 TGTATACCAACAGATGAACCTATAGCATATTTGTGATTTCTACTTTTTTTTTT

Db 213 TGTATACCAACAGATGAACCTATAGCATATTTGTGATTTCTACTTTTTTTTTT

Qy 727 TACTGTACTTTTACTATATAAACCAAGTGCACCTTTCT-CCAAAGTGTGATTTGC

Db 154 TACTGTACTTTTACTATATAAACCAAGTGCACCTTTCTCCCAAGTGTGATTTGC

Qy 786 CCTATGAGAAGATATTTTGTATCT-CGCCAATACATTGATTTTGGTATAATA

Db 94 CCTATGAGAAGATATTTTGTATCTCCGCCAATACATTGATTTTGGTATAATA

Qy 845 GCTGTTTGTCAAACCTTAAAAAAGTGCACCTTTCTCCCAAGTGTGATTTGC

Db 34 GCTGTTTGTCAAACCTTAAAAAAGTGCACCTTTCTCCCAAGTGTGATTTGC

RESULT 8

EC939267/c

LOCUS

DEFINITION

clone n10. y1 Normal Human Trabecular Bone Cells Homo sap

clone NHTBC_cn31e10 random, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Medical Genetics Branch

National Human Genome Research Institute

10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267

Tel: 301-402-4877

Fax: 301-496-7157

Email: libin@helix.nih.gov

DNA Sequencing and analyses by National Institutes of H

Intramural Sequencing Center (NISC).

Plate: 31 row: e column: 10

Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers

1. .618

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="NHTBC_cn31e10"

/sex="Female"

/tissue_type="Bone"

/cell_type="Trabecular Bone Cells"

/lab_host="SURE"

/clone_lib="Normal Human Trabecular Bone Cells"

/note="Organ: Hip; Vector: pBluescript; Site_1: EcoRI;
Library constructed by Dr. Marian Young and Dr. Pamela
Gehron Robey (NIDCR)"

66.2%; Score 600; DB 12; Length 618;
ilarity 99.8%; Pred. No. 2.1e-68;
Conservative 0; Mismatches 0; Indels 1; Gaps 1;
AGCGGACACAAATGAAGGCGACCCCAATGGTTTGTCTGTGGTGGGCAAGTCAT 300
AGCGGACACAAATGAAGGCGACCCCAATGGTTTGTCTGTGGTGGGCAAGTCAT 559
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AAGGCTAGACATTGCTATGACAGATATGTCCTCGAGAAAACCGGAAAAGTAGTTAT 499
CCCTTCATTGTCATCGGAAGGAGGCTATGACAGAGGCAAGATTCACCGGATGC 420
CCCTTCATTGTCATCGGAAGGAGGCTATGACAGAGGCAAGATTCACCGGATGC 439
CATTGATTTTGTGAGATTGAACCTTTATGCTGTGACCAAGGACACGAGCATTGAGAC 480
CATTGATTTTGTGAGATTGAACCTTTATGCTGTGACCAAGGACACGAGCATTGAGAC 379
TTAAACAATAGACATGGAACAATGACAGGAGCTCTCTAAAGCGGAGATAAACCTCTA 540
TTAAACAATAGACATGGAACAATGACAGGAGCTCTCTAAAGCGGAGATAAACCTCTA 319
TGCAAGGGGAATTTGAAAAGATGAGAGCCAGCTGACAGTCTATACAGATGTCAGT 600
TGCAAGGGGAATTTGAAAAGATGAGAGCCAGCTGACAGTCTATACAGATGTCAGT 259
TAGAAGATATTTTAAAGAAATGACCATGATGCTGATGCTTCATTCTCCCAAGGA 660
TAGAAGATATTTTAAAGAAATGACCATGATGCTGATGCTTCATTCTCCCAAGGA 199
ACAATGTATACCAACACGATGAACCTATGACATATTTGTTCTAC -TTTTTTTTTA 140
TATTTACTGACTTTTATGATATAACCAAGTCTCTTCTCCCAAGTGTATTTGCTAT 780
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AGGCTGTTTT 852
|||||
AGGCTGTTTT 8

4396 734 bp mRNA linear EST 20-OCT-2000
88821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891173 5',
sequence.

4396
4396.1 GI:10323172

sapiens (human)
sapiens
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
bases 1 to 734)

MGC <http://mgi.nci.nih.gov/>.
onal Institutes of Health, Mammalian Gene Collection (MGC)
blished (1999)
act: Robert Strausberg, Ph.D.
l: cgabbs-remail.nih.gov
ue Procurement: DCTD/DP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LL
DNA Sequencing by: Inocyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM9675 row: j column: 06
High quality sequence stop: 602.

Location/Qualifiers
1. 734

FEATURES
source

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/clone_lib="NIH_MGC_69"
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Site 2: SalI; Cloned unidirectionally. Primer
Average insert size 1.1 kb. Library construc
Technologies."

ORIGIN

Query Match 64.5%; Score 585.2; DB 10; Length 734;
Best Local Similarity 98.3%; Pred. No. 1.5e-66;
Matches 623; Conservative 0; Mismatches 8; Indels 3;
QY 1 GAGCAGTCTTCTGCTGGAGCGATGCCAAACACCATGCTTCTTATTTCAGAT
Db 9 GAGCAGTCTTCTGCTGGAGCGATGCCAAACACCATGCTTCTTATTTCAGAT
QY 61 TTTCTTTTATCTGTGGGCGCTTTTACTGCTCAGAGACAAAGAAAGAGGAGAG
Db 69 TTTCTTTTATCTGTGGGCGCTTTTACTGCTCAGAGACAAAGAAAGAGGAGAG
QY 121 AGAGTGAATAATGAGATTTTGCATGCTCCAGAAATCTGCTCTAAGAACAAGCA
Db 129 AGAGTGAATAATGAGATTTTGCATGCTCCAGAAATCTGCTCTAAGAACAAGCA
QY 181 AGACCTACTAATGCCATTTATGAGCGCTACCTGGCTAAAGCGCTCGAAT
Db 189 AGACCTACTAATGCCATTTATGAGCGCTACCTGGCTAAAGCGCTCGAAT
QY 241 CAGCGGACACAAATGAAGGCCACCCCAATGGTTTCTTCTTGGTGTGGGCG
Db 249 CAGCGGACACAAATGAAGGCCACCCCAATGGTTTCTTCTTGGTGTGGGCG
QY 301 AAAAGGCGCTAGACATTTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAG
Db 309 AAAAGGCGCTAGACATTTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAG
QY 361 ACCCGCTTCTTCTATGACAGAGGAGGCTATGCGAAGGCAAGATTCCAC
Db 369 ACCCGCTTCTTCTATGACAGAGGAGGCTATGCGAAGGCAAGATTCCAC
QY 421 TACATTGATTTT -TTGAGATTGAACTTTATGCTGTGACCAAGGACCGAGAGCF
Db 429 TACATTGATTTTCTTGAGATTGAACTTTATGCTGTGACCAAGGACCGAGAGCF
QY 480 CATTTAACAATAAGACATGGAACAATGACAGGCGAGCTCTCTTAAAGCCGAGATA
Db 489 CATTTAACAATAAGACATGGAACAATGACAGGCGAGCTCTCTTAAAGCCGAGATA
QY 540 ACTTGCRAAGGGAATTTGAAAAGATGAGAGCCACGCG -ACRAGTCTATATCAG
Db 549 ACTTGCRAAGGGAATTTGAAAAGATGAGAGCCACGCGTGAACAGTCTATATCAG
QY 599 GTTTTAGAAGA -TATTTTAAAGAAATGACCAT 631
Db 609 GTTTTACAGACTATCTTCAACACCACTGACCAT 642

RESULT 10


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85892                               602 bp      mRNA      linear      EST 04-SEP-2003
Zp686C11249 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
Zp686C11249 5', mRNA sequence.
85892
85892.1 GI:31949079
10 sapiens (human)
10 sapiens
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malia; Euthera; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 602)
orge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B.,
es, H.W., Weill, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
mann, S.
(Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., et al.)
ublished (2003)
tact: MIPS
S
olsraedter Landstr.1, D-85764 Neuherberg, Germany
s is the 5' sequence of the clone insert
ne from S. Wiemann, Molecular Genome Analysis, German Cancer
earch Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
uenced by EMBL (European Molecular Biology Laboratories,
delberg/Germany) within the cDNA sequencing consortium of the
man Genome Project.
s1 sequence available.
s clone (DKFZp686C11249) is available at the RZPD in Berlin.
ase contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
lin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..602
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/lab_host="DH10B"
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/note="Vector: pTriplex2; Site_1: SfiI; Site_2: SfiI;
cDNA-collection"
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Conservative 0; Mismatches 6; Indels 1; Gaps 1;
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CCCGCTCATTTGCATACGAAAGGAGGCTATGTCAGAGCGCAAGATTCACCGGATGC 420

```

primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci

by comparing gene expression profiles of hepatocellular

with those of corresponding noncancerous liver

sc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
 125106
 152456

contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 203, P. R. China
 : 86-21-50801919 (ex. 45)
 : 86-21-50801922
 il: hanzgchgc.sh.cn
 s clone is available at CHOC in Shanghai.
 Location/Qualifiers

1..690
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 XhoI"

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 Conservative 0; Mismatches 2; Indels 4; Gaps 2;

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CT 859

CT 1

96952 644 bp mRNA linear EST 06-NOV-2001

DEFINITION HOA59-1-C9.R HOA (Human Osteoarthritic Cartilage) Homo
 cDNA, mRNA sequence.

ACCESSION BG96952
 VERSION BG96952.1 GI:14307193
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 644)
 AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn
 Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., &
 Lark,M.W.

TITLE Identification and initial characterization of 5000 ex
 sequenced tags (ESTs) each from adult human normal and
 osteoarthritic cartilage cDNA libraries

JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 MEDLINE 21482651
 PUBMED 11597177

COMMENT Contact: Sanjay Kumar
 UW2109
 GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay.kumar-1@sk.com

Seq primer: T7.
 FEATURES Location/Qualifiers
 1..644

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ORIGIN

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 Best Local Similarity 99.4%; Pred. No. 9.3e-57;
 Matches 521; Conservative 0; Mismatches 2; Indels 1;
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 Db 182 TTTCTTTTATCTGTGGGGCTTTTACTGCTCAGACACAAAGAGAGGAGF
 QY 121 AGAAGTGAAAAATAGAAAGTTTTCATCGCTCCAGAAAACTGCTCTAAGACAAGCA
 Db 242 AGAAGTGAAAAATAGAAAGTTTTCATCGCTCCAGAAAACTGCTCTAAGACAAGCA
 QY 181 AGACCTACTAAATGCCATATGACGGCTACCTGGCTAAAGACGGCTCGAAAT
 Db 302 AGACCTACTAAATGCCATATGACGGCTACCTGGCTAAAGACGGCTCGAAAT
 QY 241 CAGCCGGACACAAATGAAGGCCACCCCAATGGTTTGTCTTGGTGTGGGC
 Db 362 CAGCCGGACACAAATGAAGGCCACCCCAATGGTTTGTCTTGGTGTGGGC
 QY 301 AAAAGGCTTAGACATTTGCTATGACAGATATGTCCTCGAGAAAAAGCGGAAAG
 Db 422 AAAAGGCTTAGACATTTGCTATGACAGATATGTCCTCGAGAAAAAGCGGAAAG
 QY 361 ACCCCTTCATTGCTACCGAAAGAGGCTATGACAGAGGCAAGATTCAC
 Db 482 ACCCCTTCATTGCTACCGAAAGAGGCTATGACAGAGGCAAGATTCAC
 QY 421 TACATTGATTTTGGATTGAATTTATGCTGTGACCAAGGACCGGAGCA

1CATGTGATTTTGGAGTGAACCTTATGCTGTGA-CAAAGGACCACGGGGCATTGAGAC 600
 TTAAACAAATAGACATGACAAATGACAGGCGAGCTCTCTAAAG 524
 TTAAACAAATAGACATGACAAATGACAGGCGAGCTCTCTANAG 644

 4142 618 bp mRNA linear EST 21-OCT-2003
 4142 22 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
 4142.1 GI:37798703
 scrofa (pig)
 scrofa
 uyotia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 alia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 bases 1 to 618)
 h, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
 eman, D.J., Wray, J.E. and Keele, J.W.
 line EST collection using a normalized library constructed from
 yos representing early developmental stages
 blished (2003)
 act: Smith TPL
 . ARS, US Meat Animal Research Center
 ox 166, Clay Center, NE 68933-0166, USA
 402 762 4366
 402 762 4390
 l: smith@mail.marc.usda.gov
 le pass sequencing. Bases called with phred v0.020425.c and
 med with the aid of the trim_alt option. Vector identified with
 s_match v0.990329.
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 Location/Qualifiers
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 Library made with combined RNA from day-10, day-13,
 day-15, day-25, and day-30 whole embryos."

 55.4%; Score 502.2; DB 14; Length 618;
 ilarity 89.6%; Pred. No. 8.1e-56;
 Conservative 0; Mismatches 63; Indels 0; Gaps 0;
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 3GTGGCCGTCTGGGCGGACTCCAGCATCATGCAATTTTATTAGATTAACTAATTT 75
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 TTTTACGTGTGGGGCATTTTACTGCTCAGGACAAAGACAGAGAGAGACAGAGG 135
 GTGAAATAGAGATTTTTCATGCTCCAGAAACTGCTCTAGACAAAGCAAGAGGGAG 182
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 TTAATAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAATTTCTACTGCA 242
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 TGCCTAGACATTGCTATGACAGATATGTCCTGGAGAAAGCGAAAGTAGTTATAC 362

Db 316 AAGGCTAGACATTTGCCATGATGATATGTCCTGGAGAGAGCGAAAGTG
 QY 363 CCCCTTCATTTTCATACCGAAAGAGGCTATGCGAAGCGAAGATTCCACCG
 Db 376 CCCCTTCCTTTTCATATGGAAGAGGCTATGCGAAGCAAGATTCCACCT
 QY 423 CATTGATTTTTCAGATTTGAACCTTTATGCTGTGACCAAGGACCGAGCATTT
 Db 436 CATTGATTTTTCAGATTTGAACCTTTATGCTGTGACCAAGGACCGAGCATTT
 QY 483 TTAAACAAATAGACATGACAGGACATGACAGCAACTCTCTAAACTGAGATTAAT
 Db 496 TTAAACAGATAGACAGGACATGACAGCAACTCTCTAAACTGAGATTAAT
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 Db 556 TGAAGAGGAATTTGAAAGAGATGAGAGCCACGTCGACAAATCATATCAGAT
 QY 603 TAG 605
 Db 616 TAG 618

Search completed: April 9, 2004, 10:38:56
 Job time : 3244 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004, Compugen Ltd.

leic search, using sw model

April 9, 2004, 08:30:30 ; Search time 417 Seconds
(without alignments)
8159.654 Million cell updates/sec

US-10-015-480A-179

907

1 gagcagtggtctgtgtggagc.....aaaaaaaaaaaaaaaaaaaaa 907

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

2475585 seqs, 1875730760 residues

hits satisfying chosen parameters: 4951170

ength: 0

ength: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Published Applications NA:*
- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
 - 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
 - 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
 - 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
 - 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
 - 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
 - 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
 - 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
 - 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
 - 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
 - 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
 - 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
 - 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
 - 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
 - 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
 - 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
 - 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
 - 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query Match	Length	DB ID	Description
100.0	907	10	US-09-946-374-179
100.0	907	14	Sequence 179, App
100.0	907	14	Sequence 179, App
100.0	907	14	US-10-006-856A-179
100.0	907	14	Sequence 179, App
100.0	907	14	US-10-006-818A-179
100.0	907	14	Sequence 179, App
100.0	907	14	US-10-015-393A-179
100.0	907	14	Sequence 179, App
100.0	907	14	US-10-015-869A-179
100.0	907	14	Sequence 179, App
100.0	907	14	US-10-012-121A-179
100.0	907	14	Sequence 179, App
100.0	907	14	US-10-006-116A-179
100.0	907	14	Sequence 179, App
100.0	907	14	US-10-006-117A-179
100.0	907	14	Sequence 179, App
100.0	907	14	US-10-017-527A-179
100.0	907	14	Sequence 179, App
100.0	907	14	US-10-013-913A-179
100.0	907	14	Sequence 179, App
100.0	907	14	US-10-007-194A-179
100.0	907	14	Sequence 179, App
100.0	907	14	US-10-013-430A-179
100.0	907	14	Sequence 179, App
100.0	907	14	US-10-011-671A-179
100.0	907	14	Sequence 179, App
100.0	907	14	US-10-012-755A-179
100.0	907	14	Sequence 179, App
100.0	907	14	US-10-015-386A-179
100.0	907	14	Sequence 179, App

16	907	100.0	907	14	US-10-011-692A-179	Sequen
17	907	100.0	907	14	US-10-006-768A-179	Sequen
18	907	100.0	907	14	US-10-017-610A-179	Sequen
19	907	100.0	907	14	US-10-006-063A-179	Sequen
20	907	100.0	907	14	US-10-020-063A-179	Sequen
21	907	100.0	907	14	US-10-015-391A-179	Sequen
22	907	100.0	907	14	US-10-017-407A-179	Sequen
23	907	100.0	907	14	US-10-011-833A-179	Sequen
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25	907	100.0	907	14	US-10-015-822A-179	Sequen
26	907	100.0	907	14	US-10-015-387A-179	Sequen
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40	907	100.0	907	14	US-10-013-910A-179	Sequen
41	907	100.0	907	14	US-10-013-911A-179	Sequen
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44	907	100.0	907	14	US-10-012-101B-179	Sequen
45	907	100.0	907	14	US-10-015-480A-179	Sequen

ALIGNMENTS

RESULT 1
US-09-946-374-179
; Sequence 179, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and N
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750

[illegible]

Identity	Conservative	Score	DB 10	Length	907
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100.0%;	0;	Pred. No. 3.5e-181;			
Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;	
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 AAAAAA 907
 AAAAAA 907

179 Application US/10006818A
 C. US2003005406A1

VATION:

aker, Kevin P.
 Botstein, David
 Desnoyers, Luc
 Eaton, Dan L.
 Ferrara, Napoleone
 Fong, Sherman
 Rao, Wei-Qiang
 Soddard, Audrey
 Sodowski, Paul J.
 Strimaldi, Christopher J.
 Burney, Austin L.
 Hillan, Kenneth J.
 Pan, James
 Paoni, Nicholas F.

ENITION: Secreted and Transmembrane Polypeptides and Nucleic
 ENITION: Acids Encoding the Same

CE: P2830P1C4

ICATION NUMBER: US/10/006,818A

NG DATE: 2001-12-06

ation removed - See File Wrapper or Palm

2 ID NOS: 477

US-10-006-818A-179

Query Match	100.0%	Score 907;	DB 14;	Length 907;
Best Local Similarity	100.0%	Pred. No. 3.5e-181;		
Matches 907;	Conservative 0;	Mismatches 0;	Indels 0	
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Db	301	AAAGGCCCTAGACATTTGCTATGACAGATATGCTGCTTAAAGAGGCAAGTCCAC		
Qy	361	ACCCCTTTCATTTGCTATGACAGATATGCTGCTTAAAGAGGCAAGTCCAC		
Db	361	ACCCCTTTCATTTGCTATGACAGATATGCTGCTTAAAGAGGCAAGTCCAC		
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Qy	781	TTTTCCCTATGAGAGATATTTTGTATCTCCCAATACATTTGATTTTGGTATA		
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Db	841	TGAGGCTGTTTGGCAACCTTAAACAAACAAACAAACAAACAAACAAACAAAC		
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Db	901	AAAAAA 907		

RESULT 4
 US-10-015-393A-179

omo sapiens

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179 Application US/10012121A
3. US20030073810A1
WATION:
aker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Soo, Wei-Qiang
Boddard, Audrey
Jodowski, Paul J.
Zrimaldi, Christopher J.
Surney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/10/012,121A
CURRENT FILING DATE: 2001-12-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 179
LENGTH: 907
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-121A-179

Query Match 100.0%; Score 907; DB 14; Length 907;
Best Local Similarity 100.0%; Pred. No. 3.5e-181; Indels 0;
Matches 907; Conservative 0; Mismatches 0; Indels 0;
QY 1 GAGCAGTGTCTGCTGGAGCCGATGCCAAAACCATGCAATTTCTTATTCAGAG 907
DB 1 GAGCAGTGTCTGCTGGAGCCGATGCCAAAACCATGCAATTTCTTATTCAGAG 907
QY 61 TTTCTTTTATCTGTTGGGCTTTTCTGCTGAGAGCAAAAGAGAGAGAG 907
DB 61 TTTCTTTTATCTGTTGGGCTTTTCTGCTGAGAGCAAAAGAGAGAGAG 907
QY 121 AGAAGTGAAATAGAAAGTTTTCATGCTGCTGAGAGCAAAAGAGAGAGAG 907
DB 121 AGAAGTGAAATAGAAAGTTTTCATGCTGCTGAGAGCAAAAGAGAGAGAG 907
QY 181 AGACCTACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGAGCGGCTCGAAAT 907
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QY 241 CAGCCGGACACAAATGAAGCCACCCCAATGTTTCTTCTGTTGGTGGG 907
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DB 481 ATTAAACAAATAGACATTTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 907
QY 541 CTGCAAGGAGATTTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
DB 541 CTGCAAGGAGATTTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
QY 601 TTTAGAAGATATTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
DB 601 TTTAGAAGATATTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
QY 661 ATACAATGTATACCAACAGATGAACTATGACATTTGATTTCTTCTTCTTCT 907
DB 661 ATACAATGTATACCAACAGATGAACTATGACATTTGATTTCTTCTTCTTCT 907
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DB 721 GCTATTTACTGTACTTTTATGATTAATAAAAGAGAGAGAGAGAGAGAGAGAG 907
QY 781 TTTTCCCTCTGAGAGAGATATTTGATCTCCCAATACATTTGATTTGATTTG 907
DB 781 TTTTCCCTCTGAGAGAGATATTTGATCTCCCAATACATTTGATTTGATTTG 907

us-10-015-480a-179.rnpb

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 GAGCGTGTGTTGCACACTTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 900

AAAAAA 907
 |||||
 AAAAAA 907

179 Application US/10006116A
 o. US20030082626A1
 MATION:
 Baker, Kevin P.
 Botstein, David
 Desnoyers, Luc
 Saton, Dan L.
 Ferrara, Napoleone
 Fong, Sherman
 Bao, Wei-Qiang
 Joddard, Audrey
 Sodowski, Paul J.
 Primaldi, Christopher J.
 Burney, Austin L.
 Hillan, Kenneth J.
 An, James
 Aoni, Nicholas F.

ENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ENITION: Acids Encoding the Same
 E: P283PIC15
 CATION NUMBER: US/10/006,116A
 G DATE: 2001-12-16
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 ATION NUMBER: 60/106023
 DATE: 1998-10-28

100.0%; Score 907; DB 14; Length 907;
 Nilarity 100.0%; Pred. No. 3.5e-181;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGCAGTGTCTGCTGGAGCCGATGCCAAAACCATGCAATTCCTATTTCAGATTCAATCT 60
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 Db 61 TTTCTTTTATCTCTGGGGCCTTTTCTCTCTCAGAGCAAAAAGAGAGAGGAGG
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 QY 121 AGAAGTGAATAATAGAAAGTTTTCATCGTCCAGAAAACTGCTCTAAGACAAGCF
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 Db 121 AGAAGTGAATAATAGAAAGTTTTCATCGTCCAGAAAACTGCTCTAAGACAAGCF
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 QY 181 AGACCTACTAAATGCCCATTTATGACGGCTACCTGGCTTAAGACGGCTCGAAAT
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 Db 181 AGACCTACTAAATGCCCATTTATGACGGCTACCTGGCTTAAGACGGCTCGAAAT
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 QY 241 CAGCCGGACACAAAATGAAGGCCACCCCAAAATGGTTTGTCTTGGTGTGGGG
 |||||
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 QY 301 AAAAGGCTAGACATTTGCTATGACAGATATGTCCTCGAGAAAAAGCGAAAG
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 Db 301 AAAAGGCTAGACATTTGCTATGACAGATATGTCCTCGAGAAAAAGCGAAAG
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 Db 361 ACCCCCTTCATTTGCATACGGAAGGAAGGCTATGACAGAGGCAAGATTCCAC
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 Db 421 TACATTGATTTTGGAGATTGAACTTTATGCTGTGACCAAAAGGACCGAGGCA
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 |||||
 Db 481 ATTAAACAAATAGACATGGAATGACAGCAATGACAGGCGAGCTCTCTAAAGCCGAGATA
 |||||
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 Db 541 CTTGCAAGGGAATTTGAAAAGATGAGAAAGGACCAAGTCAATATCAGG
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 QY 661 ATACAATGTATACCAACACGATGAATAGCAATATTTGATTTTCTACCTTTT
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 Db 661 ATACAATGTATACCAACACGATGAATAGCAATATTTGATTTTCTACCTTTT
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 QY 841 TGAGGCTGTTTGGCAAACTTAAAAAATAAAAAAATAAAAAAATAAAAAA
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 QY 901 AAAAAA 907
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 Db 901 AAAAAA 907
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RESULT 8

US-10-006-117A-179
 ; Sequence 179, Application US/10006117A
 ; Publication No. JS20030082627A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman

iao, Wei-Qiang
 Goddard, Audrey
 Grimaldi, Paul J.
 Grimaldi, Christopher J.
 Gurney, Austin L.
 Hillan, Kenneth J.
 Pan, James
 Paoni, Nicholas F.
 ACTION: Secreted and Transmembrane Polypeptides and Nucleic
 ACTION: Acids Encoding the Same
 E: P2830P1C13
 CATION NUMBER: US/10/006,117A
 IG DATE: 2002-03-19
 tion removed - See File Wrapper or Palm
 DATE: 2001-07-09
 ID NOS: 477

mo sapiens
 79

100.0%; Score 907; DB 14; Length 907;
 ilarity 100.0%; Pred. No. 3.5e-181; Indels 0; Gaps 0;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 AAGTCAAAATAGAAAGTTTGGCATGCTCCAGAAAACCTGCTTAAGCAAGCAGAGAGG 180
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 ACCTACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTTCTACTG 240
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 SCCGACACAAATAGAGCCACCCCAATAGTTGTTCTTGGTGTGGGCAAGTCAT 300
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 DB 721 GCTATTACTGTACTTTATGTATATAAAACAAAGTCACATTTCTCCAAAGTTGTAT
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 US-10-017-527A-179
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 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
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 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and N
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830P1C63
 ; CURRENT APPLICATION NUMBER: US/10/017,527A
 ; CURRENT FILING DATE: 2001-12-13
 ; PRIOR APPLICATION NUMBER: 60/098716
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72	PRIOR FILING DATE: 1998-10-27
73	PRIOR APPLICATION NUMBER: 60/106023

DATE: 1998-10-28
100.0%; Score 907; DB 14; Length 907;
milarity 100.0%; Pred. No. 3.5e-181;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AAAAA 907

Sequence 179, Application US/10013913A
Publication No. US20030083462A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C40
CURRENT APPLICATION NUMBER: US/10/013,913A
CURRENT FILING DATE: 2002-07-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 179
LENGTH: 907
TYPE: DNA
ORGANISM: Homo sapiens
US-10-013-913A-179

Query Match 100.0%; Score 907; DB 14; Length 907;
Best Local Similarity 100.0%; Pred. No. 3.5e-181;
Matches 907; Conservative 0; Mismatches 0; Indels 0;
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DB 1 GAGCAGTGTCTGCTGAGCGGATGCCAAACCATCATCTTCTATTCAGAT
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DB 61 TTCTTTATCTGCTGCGGCGCTTTTACTGCTCAGACACAAAGAGAGGAGGAG
121 AGAAGTGAATAATAGAAATTTTGCATGCTCCAGAAAACCTCTTAAGACAAAGCA
121 AGAAGTGAATAATAGAAATTTTGCATGCTCCAGAAAACCTCTTAAGACAAAGCA
181 AGACCTACTAAATGCCATTTATGACGGCTA CTTGGCTAAAGACGGCTCGAAAT
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241 CAGCGGACACAAATGAAGGCCACCCCAATGGTTTCTTGGTGTGGGCT
241 CAGCGGACACAAATGAAGGCCACCCCAATGGTTTCTTGGTGTGGGCT
301 AAAAGGCTCAGACATTTGCTATGACAGATATGTCCTGGAGAAAAGCGAAAAGT
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361 ACCCCCTTCATTTCATACGAAAGGAGGCTATGCAAGAGGCAAGATTCACCC
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541 CTTGCAAGGGGAATTTGAAAGAGATGAGAGGCCCGTGAAGTCAATATCAGGA
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TTAGAGATATTTTAAAGAGATGACCATGATGGTGATGCTTCATTTCTCCCAAGGA 660
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AAAAAA 907
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AAAAAA 907

179
Application US/10007194A
O. US20030092061A1
MATION:
aker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan I.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
ENTION: Secreted and Transmembrane Polypeptides and Nucleic
ENTION: Acids Encoding the Same
CE: P2830P1C6
ICATION NUMBER: US/10/007,194A
NG DATE: 2002-06-25
ATION NUMBER: 60/098716
DATE: 1998-09-01
ATION NUMBER: 60/098723
DATE: 1998-09-01
ATION NUMBER: 60/098749
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ATION NUMBER: 60/098750
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ATION NUMBER: 60/098821
DATE: 1998-09-02
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ATION NUMBER: 60/099602
DATE: 1998-09-09
ATION NUMBER: 60/099642
DATE: 1998-09-24
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PRIORITY APPLICATION NUMBER: 60/101738
PRIORITY FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1998-10-26		
; PRIOR APPLICATION NUMBER: 60/105807		
; PRIOR FILING DATE: 1998-10-27		
; PRIOR APPLICATION NUMBER: 60/105881		
; PRIOR FILING DATE: 1998-10-27		
; PRIOR APPLICATION NUMBER: 60/105882		
; PRIOR FILING DATE: 1998-10-27		
; PRIOR APPLICATION NUMBER: 60/106023		
; PRIOR FILING DATE: 1998-10-28		
 Query Match 100.0%; Score 907; DB 14; Length 907;		
Best Local Similarity 100.0%; Pred. No. 3.5e-181;		
Matches 907; Conservative 0; Mismatches 0; Indels 0;		
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Dd	1	GAGCAGTGTTCCTGCTGGAGCGGATGCCAAAAACCATGCATTCTCTATTTCAGAT
Qy	61	TTTCTTTTATCTGTGGGGCCCTTTTTACTGCTCAGAGCAAAAGAAAAGAGGAGA
Dd	61	TTTCTTTTATCTGTGGGGCCCTTTTTACTGCTCAGAGCAAAAGAAAAGAGGAGA
Qy	121	AGAGTGCAAATACGAAGTTTTGTCATGCTCAGAGCAAAAGAAAAGAGGAGA
Dd	121	AGAGTGCAAATACGAAGTTTTGTCATGCTCAGAGCAAAAGAAAAGAGGAGA
Qy	181	AGACCTTACTAAATGCCCATATATCACGGCTACCTGGCTTAAGACGGCTCGAAT
Dd	181	AGACCTTACTAAATGCCCATATATCACGGCTACCTGGCTTAAGACGGCTCGAAT
Qy	241	CAGCCGGACACAATAAGAGCCACCACCACCAATGGTTGTTCTTGGTGTGGGCI
Dd	241	CAGCCGGACACAATAAGAGCCACCACCACCAATGGTTGTTCTTGGTGTGGGCI
Qy	301	AAAGSCCTTAGACATTGCTATGACAGATATGTCCTCGAGAAAAGCGAAAAG
Dd	301	AAAGSCCTTAGACATTGCTATGACAGATATGTCCTCGAGAAAAGCGAAAAG
Qy	361	ACCCCCTTCATTGTCATACGGAAGGAAGGCTATGACAGAACGCAAGATCCAC
Dd	361	ACCCCCTTCATTGTCATACGGAAGGAAGGCTATGACAGAACGCAAGATCCAC
Qy	421	TACANTGATTTTTGAGATTGAATTTATGCTGTGACCAAGGACCACCGAGCA
Dd	421	TACANTGATTTTTGAGATTGAATTTATGCTGTGACCAAGGACCACCGAGCA
Qy	481	ATTTAACAAATAGACATGGACAATGACAGGAGCTCTCTTAAGCGCGATAAF
Dd	481	ATTTAACAAATAGACATGGACAATGACAGGAGCTCTCTTAAGCGCGATAAF
Qy	541	CTTGCAAGGGGAATTTGAAAAGATGAGAAAGCCAGTGACCAAGTCATATCAGF
Dd	541	CTTGCAAGGGGAATTTGAAAAGATGAGAAAGCCAGTGACCAAGTCATATCAGF
Qy	601	TTTGAAGATATTTTTAAGAAGATGACCATGATGGTGTGATGCTTCCTCTCC
Dd	601	TTTGAAGATATTTTTAAGAAGATGACCATGATGGTGTGATGCTTCCTCTCC
Qy	661	ATACATGTATACCAACAGATGAATATAGCATATTTGATTTCTACTTTTTT
Dd	661	ATACATGTATACCAACAGATGAATATAGCATATTTGATTTCTACTTTTTT
Qy	721	GCTATTTACTGTACTTTTATGATATAAAACAAAGTCACITTTCTCCAAGTGTATT
Dd	721	GCTATTTACTGTACTTTTATGATATAAAACAAAGTCACITTTCTCCAAGTGTATT
Qy	781	TTTTCCCCCTATGAGAAGATAATTTTGATCTCCCCAATACATTTGTTGTTATAA
Dd	781	TTTTCCCCCTATGAGAAGATAATTTTGATCTCCCCAATACATTTGTTGTTATAA
Qy	841	TGAGCTGTTTTGCAACTTAAAAAIAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Dd	841	TGAGCTGTTTTGCAACTTAAAAAIAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

AAAAAA 907
||||||
AAAAAA 907

179
Application US/10013430A
o. US20030092883A1

MATION:

aker, Kevin P.

Botstein, David

Desnoyers, Luc

Eaton, Dan I.

Ferrara, Napoleone

Fong, Sherman

Gao, Wei-Qiang

Goddard, Audrey

Godowski, Paul J.

Grimaldi, Christopher J.

Gurney, Austin L.

Hillan, Kenneth J.

Pan, James

Paoni, Nicholas F.

ENTION: Secreted and Transmembrane Polypeptides and Nucleic

ENTION: Acids Encoding the Same

CE: P2830P1C31

ICATION NUMBER: US/10/013,430A

NG DATE: 2002-06-25

action removed - See File Wrapper or Palm

Q ID NOS: 477

omc sapiens
179

ilarity 100.0%; Score 907; DB 14; Length 907;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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TTCTTTTATCTGTGGGCTTTTACTGCTCAGAGACAAAGAGAGAGAGAGAGAGAG 120
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Db 481 ATTTAAACAAATAGACATGGACAATGACAGGAGCTCTCTAAAGCCGAGATAJ
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Db 541 CTTGCAAGGGAATTTGAAAAAGATGAGAGCCACGTCGACAGTCATATCAGK
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QY 661 ATACAATGTATACCAACACGATGAACCTATAGCATATTTGATTTCTACTTTT
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QY 721 GCTATTACTGTACTTTATGTATATAAAACAAAGTCACTTTTCTCCAAAGTTGTAT
Db 721 GCTATTACTGTACTTTATGTATATAAAACAAAGTCACTTTTCTCCAAAGTTGTAT
QY 781 TTTTCCCTATGAGAGAGATATTTTGTATCTCCCAATACATTTGATTTGGTATA
Db 781 TTTTCCCTATGAGAGAGATATTTTGTATCTCCCAATACATTTGATTTGGTATA
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Db 841 TGAGGCTGTGTTGCAAACTTAAAAAAGGAGAGAGAGAGAGAGAGAGAGAGAG 841
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Db 901 AAAAAA 907

RESULT 13

US-10-011-671A-179

; Sequence 179, Application US/10011671A

; Publication No. US20030096954A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan I.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C27

; CURRENT APPLICATION NUMBER: US/10/011,671A

; PRIOR FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: 60/098716

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098723

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098749

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098750

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098803

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/098821

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/098843

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/099536

DATE: 1998-09-09
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 ATION NUMBER: 60/105882
 DATE: 1998-10-27
 ATION NUMBER: 60/106023
 DATE: 1998-10-28

100.0%; Score 907; DB 14; Length 907;
 milarity 100.0%; Pred. No. 3.5e-181;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 GAAGTGAATAAGAGTGTTCGATCTGCTCCAGAAAAGTCTTAAGACAAGAGAGG 180
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 TACAATGTATACCAACAGATGACATAGCATATTTGATTTCTACTTTTTTTTAA 720
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 CTATTTTACTGTACTTTATGATAAACAAGTCACTTTTCTCCAGTTGATTTGCTAT 780

QY 781 TTTTCCCTATGAGAGATATTTTGTATCTCCCAATACATTTGTTGTTAT
 Db 781 TTTTCCCTATGAGAGATATTTTGTATCTCCCAATACATTTGTTGTTAT
 QY 841 TGAGGCTGTTTTCACAACTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA
 Db 841 TGAGGCTGTTTTCACAACTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA
 QY 901 AAAAAA 907
 Db 901 AAAAAA 907

RESULT 14
 US-10-012-755A-179
 ; Sequence 179, Application US/10012755A
 ; Publication No. US20030096955A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P28301C28
 ; CURRENT APPLICATION NUMBER: US/10/012,755A
 ; CURRENT FILING DATE: 2002-06-10
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 477
 ; SEQ ID NO 179
 ; LENGTH: 907
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-012-755A-179

Query Match 100.0%; Score 907; DB 14; Length 907;
 Best Local Similarity 100.0%; Pred. No. 3.5e-181;
 Matches 907; Conservative 0; Mismatches 0; Indels 0;

QY 1 GAGCAGTGTCTGCTGAGCGCATGCCAAAACCATGCAATTTCTTATTCAGAT
 Db 1 GAGCAGTGTCTGCTGAGCGCATGCCAAAACCATGCAATTTCTTATTCAGAT
 QY 61 TTTCTTTTATCTGTGGGCGCTTTTACTGCTCAGAGACAAAAGAGAGGAGP
 Db 61 TTTCTTTTATCTGTGGGCGCTTTTACTGCTCAGAGACAAAAGAGAGGAGP
 QY 121 AGAAGTGAATAAGAGATTTTGCATGCTCAGAGACAAAAGAGAGAGP
 Db 121 AGAAGTGAATAAGAGATTTTGCATGCTCAGAGACAAAAGAGAGAGP
 QY 181 AGACCTACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAAT
 Db 181 AGACCTACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAAT
 QY 241 CAGCCGACACAAAATGAAGGCCACCCCAATGTTTGTCTTGTGTTGGGC
 Db 241 CAGCCGACACAAAATGAAGGCCACCCCAATGTTTGTCTTGTGTTGGGC
 QY 301 AAAAGGCTAGACATTTGCTATGACAGATATGTCCTCGAGAAAAGCGAAAAG
 Db 301 AAAAGGCTAGACATTTGCTATGACAGATATGTCCTCGAGAAAAGCGAAAAG

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:CCCTTCATTTGTCATCGAAGGAGAGGCTATGAGAGGCAAGATGCCACCGATGC 420
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:CCCTTCATTTGTCATCGAAGGAGAGGCTATGAGAGGCAAGATGCCACCGATGC 420
|||||
:CATTTGATTTTGGAGTTGAACTTTATGCTGTGACCAAGGACCAAGAGCAATTTGAGAC 480
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enoyers, Luc
aton, Dan L.
errara, Napoleone
ong, Sherman
ao, Wei-Qiang
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odowski, Paul J.
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Best Local Similarity 100.0%; Pred. No. 3.5e-181;
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QY 901 AAAAAA 907
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GenCore version 5.1.6
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April 9, 2004, 07:01:20 ; Search time 480 Seconds
(without alignments)
8027.324 Million cell updates/sec

US-10-015-480A-179

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- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
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- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

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ter than or equal to the score of the result being printed,
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ALIGNMENTS

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KW cytostatic; gene therapy; vaccine; ss.
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PD 08-JUN-2000.
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PR 13-SEP-1999; 99WO-US020944.
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PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
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PA (GETH) GENENTECH INC.
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PI Ashkenazi AV, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni

Watanabe CK, Williams PM, Wood WI;

412154/35.

B24429.

ids encoding PRO polypeptides useful for preventing, diagnosing
ng diagnosing a cardiovascular, endothelial or angiogenic
in mammals.

Fig 83; 315pp; English.

t invention describes nucleic acids encoding PRO polypeptides
preventing, diagnosing and treating disorders in mammals by
ular, endothelial or angiogenic disorder in mammals by
cell proliferation, angiogenesis and cardiovascularisation,
entifying agonists and antagonists of these processes. The
ids and the proteins they encode may be used in the prevention,
and diagnosis of diseases associated with inappropriate PRO
such as cardiovascular, endothelial or angiogenic disorders in
.g. atherosclerosis, cancers and cardiac hypertrophy). For
he nucleic acids (NCs) and vectors containing them and the PRO
e may be used to treat disorders associated with decreased PRO
. AAY77510 to AAY77721 and AAB24388 to AAB24435 represent
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PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.

XX (GETH) GENENTECH INC.

Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood
MPI; 2000-237871/20.
P-FSDB; AAY99391.

New mammalian DNA sequences encoding transmembrane, receptor or
PRO polypeptides, useful for screening of potential peptide or
molecule inhibitors of the relevant receptor/ligand interaction
Claim 2; Fig 103; 773pp; English.

AAA37022 to AAA37144 encode the new isolated human transmembrane
receptor or secreted PRO polypeptides given in AAY99340 to AAY99344
transmembrane and receptor PRO proteins can be used for screening
potential peptide or small molecule inhibitors of the relevant
receptor/ligand interactions. The polypeptides and nucleotide
encoding then have various industrial applications, including
pharmaceutical and diagnostic agents. AAA37145 to AAA37330 rep
primers and hybridisation probes used in the isolation of the
polypeptides from the present invention

XX Sequence 907 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;

Query Match 100.0%; Score 907; DB 3; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.3e-155;
Matches 907; Conservative 0; Mismatches 0; Indels 0;

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Db 1 GAGCAGTGTCTCTGTCGAGCGGATGCCAAACCATGCGATTCTTATTCAGATT
Qy 61 TTTCTTTTATCTGTGGGCGCTTTTACTGCTCAGAGACAAAGAGAGAGAG
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Qy 121 AGAAGTGAATAAGAGTTTGTGTCATCGTCCAGAAAACCTGCTTAAGCAAGCAA
Db 121 AGAAGTGAATAAGAGTTTGTGTCATCGTCCAGAAAACCTGCTTAAGCAAGCAA
Qy 181 AGACCTACTAAATGCCCATTTATGACGCTACCTGGCTAAAGACGGCTCGAAATT
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Qy 241 CAGCCGACACAAAATGAAGCCACCCCAATGTTTGTCTTGTCTTGGGCA
Db 241 CAGCCGACACAAAATGAAGCCACCCCAATGTTTGTCTTGTCTTGGGCA
Qy 301 AAAAGGCTAGACATTGCTATGACAGATATGTCCTCGGAGAAAAGCGAAAGT

AAAGGCGCTAGACATTCCTATGACAGATATGTCGCCCTGGAGAAAAGCGAAAGTAGTTAT 360
 CCCCCTTCATTTGCTACCGAAGGAGGCTATGCGAAGGCGCAAGTTCCACCGATGC 420
 CCCCCTTCATTTGCTACCGAAGGAGGCTATGCGAAGGCGCAAGTTCCACCGATGC 420
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MAAAA 907

MAAAA 907

standard; DNA; 907 bp.

1 (first entry)

ag protein of the invention #52.

transmembrane; gene therapy; ss.

ad.

1-A1.

3.

0; 2000WO-US004342.

9; 99US-0141037P.

9; 99US-0144758P.

9; 99US-0145698P.

9; 99WO-US020111.

9; 99US-0162506P.

9; 99WO-US028313.

9; 99WO-US028551.

9; 99WO-US030095.

XX (GETH) GENENTECH INC.
 PA Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F
 XX Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hi
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W
 PI Williams PM, Wood WI;
 XX WPI; 2001-071395/08.
 DR

XX Secreted and transmembrane proteins and nucleic acids designat
 PT useful as hybridization probes, in chromosome and gene mapping
 PT therapy.
 PT

XX Claim 2; Fig 103; 787pp; English.

XX The present invention relates to secreted and transmembrane pr
 CC These proteins and the DNA encoding them may be used as hybrid
 CC probes, in chromosome and gene mapping and in the generation o
 CC sense RNA and DNA. They may also be used to generate eith
 CC transgenic animals or knockout animals which are in turn usefu
 CC development and screening of therapeutically useful reagents.
 CC acids may also be used in gene therapy
 XX

XX Sequence 907 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;

Query Match 100.0%; Score 907; DB 4; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.3e-155;
 Matches 907; Conservative 0; Mismatches 0; Indels 0;

QY 1 GAGCAGTGTCTGCTGGAGCCGATGCCAAAACCATGTCATTTCTTATTTCAGAT
 DB 1 GAGCAGTGTCTGCTGGAGCCGATGCCAAAACCATGTCATTTCTTATTTCAGAT

QY 61 TTCTTTTATCTGTGGGGCTTTTACTGCTCAGAGACAAAAGAGAGGAGA
 DB 61 TTCTTTTATCTGTGGGGCTTTTACTGCTCAGAGACAAAAGAGAGGAGA

QY 121 AGAAGTGAATAAGAGTTTTCATGCTCCAGAAACTGCTCTAAGACAAAGCA
 DB 121 AGAAGTGAATAAGAGTTTTCATGCTCCAGAAACTGCTCTAAGACAAAGCA

QY 181 AGACCTACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAAT
 DB 181 AGACCTACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAAT

QY 241 CAGCCGGACACAAAATGAAGGCCACCCCAATGGTTTGTCTTGGTGTGGGC
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QY 301 AAAAGCCCTAGACATTTGCTATGACAGATATGTCCTCGAGAAAGCGAAAG
 DB 301 AAAAGCCCTAGACATTTGCTATGACAGATATGTCCTCGAGAAAGCGAAAG

QY 361 ACCCCCTTCATTTGATGTTGAACCTTTATGCTGTGACCAAGGACCAAGGAGCA
 DB 361 ACCCCCTTCATTTGATGTTGAACCTTTATGCTGTGACCAAGGACCAAGGAGCA

QY 421 TACATTTGATTTTGAAGATTGAACTTTTATGCTGTGACCAAGGACCAAGGAGCA
 DB 421 TACATTTGATTTTGAAGATTGAACTTTTATGCTGTGACCAAGGACCAAGGAGCA

QY 481 ATTTAAACAAATAGACATGGGCAATGACAGGCGAGCTCTTAAAGCGGAGATAA
 DB 481 ATTTAAACAAATAGACATGGGCAATGACAGGCGAGCTCTTAAAGCGGAGATAA

QY 541 CTTGCAAGGGGAATTTGAAAAGAGATGAGAAGCCAGTGCACAGTCAATATCAGG
 DB 541 CTTGCAAGGGGAATTTGAAAAGAGATGAGAAGCCAGTGCACAGTCAATATCAGG

QY 601 TTTAAGAGATATTTTAAAGAAATGACCATGATGGTGTGATGCTTCTTCTC
 DB 601 TTTAAGAGATATTTTAAAGAAATGACCATGATGGTGTGATGCTTCTTCTC

andard; cDNA; 907 BP.

04 cDNA.

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; 2000WO-US013705.

ENTECH INC.

J, Baker KP, Ferrara N, Gerber H, Gerritsen ME;
Godowski PU, Gurney AL, Kuo SS, Mark MR, Marsters SA;
Pitti RM, Watanabe CK, Williams PM, Wood WI;

XX	WPI; 2001-025251/03.
DR	P-PSDB; AAB50960.
XX	
PT	Seventeen nucleic acids encoding PRO polypeptides which are us
PT	diagnosis and treatment of cardiovascular, endothelial or angi
PT	disorders in a mammal.
XX	
PS	Claim 60; Fig 19; 182pp; English.
XX	
CC	The present sequence is one of seventeen nucleic acids encodin
CC	polypeptides. The PRO nucleic acids, polypeptides, agonists an
CC	antagonists are useful for treating cardiovascular, endothelia
CC	angiogenic disorders in a mammal. Examples of these disorders
CC	cardiac hypertrophy, trauma, cancer, age-related macular degen
CC	atherosclerosis, hypertension, arterial restenosis, Reynaud's
CC	rheumatoid arthritis, angina, myocardial infarctions, thrombo
CC	and lymphangitis. The PRO polypeptides and antagonists are als
CC	prevent tumour angiogenesis and for treating periodontal disea
CC	are also used to stimulate wound healing and tissue regenerati
CC	nucleic acids, polypeptides and anti-PRO antibodies are useful
CC	diagnosing a cardiovascular, endothelial or angiogenic diseas
XX	
SQ	Sequence 907 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;
Query Match	100.0%; Score 907; DB 4; Length 907;
Best Local Similarity	100.0%; Pred. No. 2.3e-155;
Matches 907; Conservative	0; Mismatches 0; Indels 0;
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DB	1 GAGCAGTGTCTGCTGGAGCGCATGCCAAAACCATGCATTTCCTATTCAGAT
QY	61 TTCTCTTTATCTGTGGGGCCTTTTTACTGCTCAGACAAAAAGAAGAGAGAG
DB	61 TTCTCTTTATCTGTGGGGCCTTTTTACTGCTCAGACAAAAAGAAGAGAGAG
QY	121 AGAAGTGAAANTAGAAGTTTTGCATGCTCCAGAAAACCTCTTAAGCAAGCAJ
DB	121 AGAAGTGAAANTAGAAGTTTTGCATGCTCCAGAAAACCTCTTAAGCAAGCAJ
QY	181 AGACCTACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAAT
DB	181 AGACCTACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAAT
QY	241 CAGCCGGACACAAAATGAAGGCCACCCCATAATGGTTGTCTTGTTGGGCG
DB	241 CAGCCGGACACAAAATGAAGGCCACCCCATAATGGTTGTCTTGTTGGGCG
QY	301 AAAAGGCTTAGCATTTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGT
DB	301 AAAAGGCTTAGCATTTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGT
QY	361 ACCCCCTTCATTGTGATACGGAAAAGGAAGGCTATGCAGAAGGCCAAGATTCACA
DB	361 ACCCCCTTCATTGTGATACGGBAAAGGAGGCTATGCAGNAGSCAAGATTCACA
QY	421 TACATGTATTTTGTAGATTGAATTTATGTCTGTGACCAAAGGACCACCGAGCAT
DB	421 TACATGTATTTTGTAGATTGAACTTTATGTCTGTGACCAAAGGACCACGGAGCAJ
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DB	481 ATTTTAAACAAATAGACATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAJ
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DB	601 TTTAGAAGATATTTTAAAGAAATAGCAACCATGTATGGTGTATTCATTTCTCTC

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AAAAAA 907

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AAAAAA 907

tandard; cDNA; 907 BP.

3 (first entry)

n secreted and transmembrane protein PRO1304 cDNA.

reted and transmembrane protein; PRO; angiogenesis;
 l cell proliferation; wound healing; immune response;
 tes proliferation; neonatal heart hypertrophy; tumour;
 sufficiency disorder; calcium flux; inflammation;
 endothelial growth factor-stimulated proliferation;
 kidney mesangial cell proliferation; Berger disease;
 y; Schanlein-Henoch purpura; celiac disease; Crohn's disease;
 herpeticiformis; diabetes; haemoglobin switch; insulinaemia;
 beta-cell precursor cell differentiation; thalassemias;
 auditory hair cell regeneration; hearing loss; bone disorder;
 disorder; sports injury; arthritis; gene; ss.

ns.

30-A1.

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2000WO-US030873.
2000WO-US032678.
2001WO-US006520.
2001WO-US006666.
2001WO-US017800.
2001WO-US019692.
2001WO-US021066.
2001WO-US021735.
2001WO-US0946374.

ENTECH INC.

Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
Bard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
ni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
Wood WI;

95293/55.
33633.

XX Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418;
PT PRO1787 that modulate glucose or free fatty acid uptake by ske-
PT muscle cells, and are useful for treating diabetes, hyper- or l

Query Match 100.0%; Score 907; DB 8; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.3e-155;
Matches 907; Conservative 0; Mismatches 0; Indels 0;

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QY 661 ATCAATGTATACCAACACGATGACATATAGCATATTTGTTTCTACTTTTTT
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QY 721 GCTATTACTGTACTTTATGATATAAACAAGTCACTTTTCTCCAAAGTTGTATT
Db 721 GCTATTACTGTACTTTATGATATAAACAAGTCACTTTTCTCCAAAGTTGTATT
QY 781 TTTTCCCTATGAGAGATATTTTGTATCTCCCAATACATTTGTTTGGTATAA
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QY 841 TGAGGCTGTTTGCACAACTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
Db 841 TGAGGCTGTTTGCACAACTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
QY 901 AAAAAA 907
Db 901 AAAAAA 907

tandard; cDNA; 907 BP.

13 (first entry)

1 encoding secreted/transmembrane protein PRO1304.

gene; secreted protein; transmembrane protein; PRO; vulnery;
anidiabetic; anorectic; antihypertensive; angiogenesis; cancer;
arterial capillary; endothelial cell growth; wound healing;
T-lymphocyte proliferation; immune response suppression;
heart hypertrophy; cardiac insufficiency disorder;
endothelial growth factor; inflammation; mononuclear cell;
diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
redifferentiation; bone disorder; cartilage disorder;
ury; arthritis.

ns.

41-Al.

3.

1; 2001US-00006856.

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 3; 2001WO-US006520.
 3; 2001WO-US006666.
 3; 2001WO-US017800.
 3; 2001WO-US019692.
 3; 2001WO-US021066.
 3; 2001WO-US021735.
 3; 2001US-00946374.
 92259/46.
 144486.

VENTECH INC.

Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
 Ildard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 Imani NF, Roy MA, Smith V, Stewart RA, Tumas D, Watanabe CK;
 Li, Wood WI;

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 tem useful for treating various cardiac insufficiency
 bone and/or cartilage disorders such as sports injuries and

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 AC ACD68012;
 XX 17-SEP-2003 (first entry)
 DT 17-SEP-2003 (first entry)
 XX Novel human secreted and transmembrane protein PR01304 cDNA.
 DE Human; secreted and transmembrane protein; PRO; gene therapy;
 KW tissue typing; chromosome identification; vaccine; gene; ss.
 XX Homo sapiens.
 OS US2003073129-A1.
 EN 17-APR-2003.
 XX
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18-NOV-1998; 98US-0108858P.
18-NOV-1998; 98US-0108904P.
22-DEC-1998; 98US-00218517.
22-DEC-1998; 98US-0113266P.
30-DEC-1998; 98US-0114223P.
05-JAN-1999; 99WO-US000106.
12-APR-1999; 99US-00284291.
16-APR-1999; 99US-0129674P.
23-JUN-1999; 99US-0141037P.
20-JUL-1999; 99US-0144758P.
26-JUL-1999; 99US-0145698P.
01-SEP-1999; 99WO-US020111.
15-SEP-1999; 99WO-US021194.
18-OCT-1999; 99US-00403297.
30-NOV-1999; 99WO-US028313.
02-DEC-1999; 99WO-US028551.
16-DEC-1999; 99WO-US030095.
05-JAN-2000; 2000WO-US000219.
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11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004342.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.

0; 2000WO-US006884.
 0; 2000WO-US013705.
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 0; 2000WO-US023522.
 0; 2000WO-US023328.
 0; 2000WO-US030952.
 0; 2000WO-US030873.
 0; 2000WO-US032678.
 1; 2001WO-US006520.
 1; 2001WO-US008666.
 1; 2001US-00872035.
 1; 2001WO-US017800.
 1; 2001US-00882636.
 1; 2001WO-US019692.
 1; 2001WO-US021066.
 1; 2001WO-US021735.

NENTECH INC.

Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 Idard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 Zni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 4, Wood WI;

385292/55.
 233510.

ated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
 ion describes an isolated PRO (secreted and transmembrane)
 e (I), having at least 80% sequence identity to a sequence
 a, and as therapeutic agents e.g. vaccines.

ig 103; 561pp; English.

ilarity 100.0%; Score 907; DB 8; Length 907;
 nality 100.0%; Pred. No. 2.3e-155;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
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 DT 18-DEC-2003 (first entry)
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 KW Human; PRO; gene; ss; protein electrophoresis; chromosome mapp
 gene mapping; genetic disorder.
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 OS Homo sapiens.
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 PN US2003064925-A1.
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 PD 03-APR-2003.
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 PF 10-DEC-2001; 2001US-00013907.
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PR 30-OCT-1998; 98US-0106464P.
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PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
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PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
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PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 98US-0114223P.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
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PR 26-JUL-1999; 99US-0145698P.
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PR 29-JUN-2001; 99US-0145698P.
PR 09-JUL-2001; 99US-0145698P.
PR 04-SEP-2001; 99US-0145698P.

(GETH) GENENTECH INC.

PA Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N,
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, H
PI

oni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
Wood WI;
55602/52.
18049.

ated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
of a medicament for treating a condition responsive to PRO
, and as therapeutic agents e.g. vaccines.

3Q ID NO 179; 555pp; English.

on relates to human PRO polypeptides and the polynucleotides
em. The sequences are useful in the preparation of a
for treating a condition responsive to a PRO polypeptide. The
as are useful in a number of functional biological assays, as
weight markers for protein electrophoresis and as therapeutic

100.0%; Score 907; DB 9; Length 907;

ilarity 100.0%; Pred. No. 2.3e-155;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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TTCTTTTATCTGTGGGGCTTTTACTGCTCAGAGACAAAGAGAGAGAGACCGCA 120

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RESULT 9

ADD70694

ID ADD70694 standard; cDNA; 907 BP.

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AC ADD70694;

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DT 15-JAN-2004 (first entry)

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DE Human cDNA encoding secreted/transmembrane protein PRO1304.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
immune response; cardiac insufficiency disorder; calcium flux;
umbilical vein endothelial cell; bone disorder; cartilage diso
arthritis; wound healing; diabetes; skeletal muscle cells; obe
Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac
dermatitis; herpeticiformis; Crohn's disease; thalassaemia.

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OS Homo sapiens.

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PN US2003099625-A1.

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PD 29-MAY-2003.

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PF 12-DEC-2001; 2001US-00015385.

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PR 01-SEP-1998; 98US-0098716P.

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PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 22-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 20-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021066.
PR 04-SEP-2001; 2001WO-US021735.
XX
XX
PA (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, H
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tamas D, W
PI Williams PM, Wood WI;
XX WPI; 2003-874602/81.
DR P-PSDB; ADD70695.
XX
XX Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO141
PT PRO1787 affect glucose or free fatty acid (FFA) uptake by skel
PT cells and are useful for treating diabetes or hyper- or hypo-i
XX
PS Claim 2; SEQ ID NO 179; 553pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.3e-155;

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Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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HACCTACTAAATGCCATTATGACGGCTACCTGGCTAAGACGGCTCGAAATCTCTACTG 240
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AAAAA 907
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AAAAA 907
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Standard; cDNA; 907 BP.

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DT XX
XX
DE XX
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage diso
KW arthritis; wound healing; diabetes; skeletal muscle cells; obe
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.
XX
OS Homo sapiens.
XX
XX US2003083462-A1.
XX
XX 01-MAY-2003.
XX
XX 10-DEC-2001; 2001US-00013913.
XX
XX 05-JAN-1999; 99WO-US000106.
XX 01-SEP-1999; 99WO-US020111.
XX 15-SEP-1999; 99WO-US021194.
XX 30-NOV-1999; 99WO-US028313.
XX 02-DEC-1999; 99WO-US028551.
XX 16-DEC-1999; 99WO-US030095.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004342.
XX 24-FEB-2000; 2000WO-US005004.
XX 02-MAR-2000; 2000WO-US005841.
XX 15-MAR-2000; 2000WO-US006884.
XX 17-MAY-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 30-MAY-2000; 2000WO-US014941.
XX 02-JUN-2000; 2000WO-US015264.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
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XX 10-NOV-2000; 2000WO-US030873.
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XX 28-FEB-2001; 2001WO-US006520.
XX 01-MAR-2001; 2001WO-US006666.
XX 01-JUN-2001; 2001WO-US017800.
XX 20-JUN-2001; 2001WO-US019692.
XX 29-JUN-2001; 2001WO-US021086.
XX 09-JUL-2001; 2001WO-US021735.
XX 04-SEP-2001; 2001US-00946374.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hi
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W
XX Williams PM, Wood WI;
XX
XX WPI: 2003-755122/71.
XX P-PADB; ADD39772.
XX
XX New secreted and transmembrane PRO polypeptides useful for trea
XX cancers, kidney disorders, Crohn's disease, diabetes mellitus,
XX hypo-insulinemia, sports injuries and arthritis.
XX
XX Claim 2; SEQ ID NO 179; 557pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted
XX transmembrane protein) having at least 80% amino acid sequence
XX to an amino acid sequence chosen from 123 fully defined sequen
XX given in the specification (including their extracellular doma
XX or without their associated signal peptides. Also include are t
XX nucleotide (NA) sequences encoding PRO, a vector comprising the
XX host cell comprising the vector, producing PRO, a chimaeric mo
XX comprising PRO fused to a heterologous amino acid sequence, and
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dy. Pro is useful as molecular weight markers for protein
 .thesis and also for chromosome identification. PRO is also
 .tissue typing. PRO and PRO NA are useful as hybridisation
 . a cDNA library to isolate the full-length PRO cDNA. PRO NA is
 . generating transgenic animals or knock-out animals which are
 . development and screening useful reagents. PRO NA is also
 . gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
 . treating cancerous tumours. PRO1250, PRO1418 and PRO1410
 .les are useful for suppressing immune response. PRO1246
 .le is useful for treating cardiac insufficiency disorders.
 .lypeptide is also useful for treating tumours. PRO1246 and
 .lypeptide are useful for stimulating calcium flux in human
 . vein endothelial cells. PRO1265, PRO1250 and PRO1474
 .les are useful for treating bone and/or cartilage disorders
 .hritis) and wound healing. PRO1130, PRO1275 and PRO1418
 .les are useful for treating diabetes in skeletal muscle cells
 .y. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
 .rger disease or other nephropathies associated with Schönlain-
 .pura, coeliac disease, dermatitis, herpeticiformis or Crohn's
 .PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
 .d PRO1575 are useful in treating thalassaemias. The present
 .ncodes a PRO protein of the invention.

107 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;

100.0%; Score 907; DB 9; Length 907;

ilarity 100.0%; Pred. No. 2.3e-155;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Qy 721 GCTATTTACTGTACTTTATGTATATAAAACAAAGTCACATTTTCTCCAAGTTGTA
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 Qy 901 AAAAAA 907
 Db 901 AAAAAA 907
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 ID ADD70217 standard; cDNA; 907 BP.
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 AC ADD70217;
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 DT 15-JAN-2004 (first entry)
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 Human cDNA encoding secreted/transmembrane protein PRO1304.
 Human; ss; gene; secreted protein; transmembrane protein; PRO
 immune response; cardiac insufficiency disorder; calcium flux
 umbilical vein endothelial cell; bone disorder; cartilage dis
 arthritis; wound healing; diabetes; skeletal muscle cells; ob
 Berger disease; nephropathy; Schönlain-Henoch purpura; coelia
 dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
 Homo sapiens.
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 20-MAR-2003.
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 06-DEC-2001; 2001US-00006818.
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 PR 30-DEC-1998; 98US-0114223P.
 PR 05-JAN-1999; 99WO-US000106.
 PR 16-APR-1999; 98US-0129674P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 98US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
 PR 29-OCT-1999; 98US-0162508P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.

(GETH) GENENTECH INC.

Baker KP, Borstein D, Deanovers L, Eaton DL, Ferrara N, F
 Gao W, Goddard A, Godowski RJ, Grimaldi JC, Gurney AL, Hi
 Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W
 Williams PW, Wood W;

WPI: 2003-708344/67.
 P-PSDB; ADD70218.

Novel isolated PRO polypeptide useful for tissue typing, modul
 biological activity of cell, as molecular weight markers in pr
 electrophoresis, for treating arthritis, tumor.

37 98US-0101738P.
 37 98US-0101741P.
 37 98US-0101915P.
 37 98US-0101916P.
 37 98US-0102207P.
 37 98US-0102240P.
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 37 98US-0102570P.
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 PR 18-NOV-1998; 98US-0108904P.
 PR 22-DEC-1998; 98US-0113296P.
 PR 30-DEC-1998; 98US-0114223P.
 PR 05-JAN-1999; 99WO-US000106.
 PR 16-APR-1999; 99US-0129674P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
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 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
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 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
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 PR 23-AUG-2000; 2000WO-US021522.
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 PR 10-NOV-2000; 2000WO-US030873.
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 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.

(GETH) GENENTECH INC.

PA Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hi
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W
 PI Williams PM, Wood WL;
 XX WPI; 2003-787000/74.
 DR P-PSDB; ADD38339.

XX Novel isolated PRO polypeptide, useful for treating cancerous
 PT cardiac insufficiency disorders, wound healing, diabetes melli
 PT thalassemias.

XX Claim 2; SEQ ID NO 179; 556pp; English.

CC The invention relates to an isolated PRO polypeptide (secreted
 CC transmembrane protein) having at least 80% amino acid sequence

Query Match 100.0%; Score 907; DB 9; Length 907;
 Best Local Similarity 100.0%; Pred. No. 2.3e-155;
 Matches 907; Conservative 0; Mismatches 0; Indels 0;

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standard; cDNA; 907 BP.

34 (first entry)

A encoding secreted/transmembrane protein PRO1304.

; gene; secreted protein; transmembrane protein; PRO; tumour;
sponse; cardiac insufficiency disorder; calcium flux;
vein endothelial cell; bone disorder; cartilage disorder;
; wound healing; diabetes; skeletal muscle cells; obesity;
sease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
s; herpetiformis; Crohn's disease; thalassaemia.

ens.

US2003096954-A1.

22-MAY-2003.

07-DEC-2001; 2001US-00011671.

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XX 07-OCT-1998; 98US-0103314P.

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72: 2000WO-US000376.
73: 2000WO-US003565.
74: 2000WO-US004342.

24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
15-MAR-2000; 2000WO-US006884.
17-MAY-2000; 2000WO-US013795.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
23-AUG-2000; 2000WO-US023522.
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08-NOV-2000; 2000WO-US030952.
10-NOV-2000; 2000WO-US030873.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
29-JUL-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
04-SEP-2001; 2001US-00946374.

XX
PA (GUTH ) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hi
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W
PI Williams FM, Wood WI;
XX
DR WPI; 2003-786999/74.
DR P-PSDB; ADD39295.
XX
XX
PT Novel isolated PRO polypeptide useful for tissue typing, modul
PT biological activity of cell, as molecular weight markers in pr
PT electrophoresis, for treating arthritis, tumor.
XX
PS Claim 2; SEQ ID NO 179; 550pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted

Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.3e-155;
Matches 907; Conservative 0; Mismatches 0; Indels 0;

QY 1 GAGCAGTGTTCGTGGAGCCGATGCCAAAACCATGCAATTCCTTATTCCAGAT
DB 1 GAGCAGTGTTCGTGGAGCCGATGCCAAAACCATGCAATTCCTTATTCCAGAT
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us-10-015-480a-179.rng

standard: cDNA: 907 BP.

PA	(GETH) GENENTECH INC.	
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PI	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F	
PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hi	
PI	Pan J, Paoni NP, Roy MA, Smith V, Stewart TA, Tumas D, W	
PI	Williams PM, Wood WI;	
XX	WPI; 2003-765477/72.	
DR	P-PSDB; ADD38818.	
XX		
DR		
XX		
PT	New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018,	
PT	PRO1244, PRO1246, useful for treating cancerous tumors, cardia	
PT	insufficiency disorders, wound healing, Crohn's disease, cellia	
XX	Claim 2; SEQ ID NO 179; 555pp; English.	
XX		
CC	The invention relates to an isolated PRO polypeptide (secreted	
	Query Match 100.0%; Score 907; DB 9; Length 907;	
	Best Local Similarity 100.0%; Pred. No. 2.3e-155;	
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QY	121 AGAAGTGAAATAGAAAGTTTGTGCATCGTCAGAAAACTGCTCTAAGACAAGCA	
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DB	181 AGACCTTACTAAATGCCCATTTATCAGCGCTACCTGGCTTAAGACGGCTCGAAAT	
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QY	301 AAAAGGCGCTAGACATTTGCTATGACAGATATGTCCTTGAGAAAAGCGAAAAG	
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AAAAAA 907

standard; cDNA; 907 BP.

4 (first entry)

encoding secreted/transmembrane protein PRO1304.

gene; secreted protein; transmembrane protein; PRO; tumour;
poinse; cardiac insufficiency disorder; calcium flux;
vein endothelial cell; bone disorder; cartilage disorder;
wound healing; diabetes; skeletal muscle cells; obesity;
sease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
;; herpeticiformis; Crohn's disease; thalassaemia.

ns.

;27-A1.

13.

11; 2001US-00006117.

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 2001WO-US021735.
 2001US-00946374.

VENTECH INC.

Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
 idard A, Godowski RJ, Grimaldi JC, Gurney AL, Hillan KJ;
 ni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 4, Wood WI;

755104/71.
 240249.

ad PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,
 RO1246, are useful for treating cancerous tumors and cardiac
 ncy disorders.

EQ ID NO 179; 550pp; English.

ion relates to an isolated PRO polypeptide (secreted or

nilarity 100.0%; Score 907; DB 9; Length 907;
 nilarity 100.0%; Pred. No. 2.3e-155;

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10:32:15 2004

us-10-015-480a-179.rge

Nickol
10/015480
Seq. IDs 179

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using sw model

April 9, 2004, 07:02:32 ; Search time 3954 Seconds
(without alignments)
9942.370 Million cell updates/sec

US-10-015-480A-179

907

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IDENTITY NUC

Gapop 10.0 , Gapext 1.0

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Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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is the number of results predicted by chance to have a

score greater than or equal to the score of the result being I
and is derived by analysis of the total score distribution.

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6	861.6	95.0	968	6	BD193126	BD193126
7	762	84.0	1067	9	AF100751	AF100751
8	669	73.8	669	9	BT007122	BT007122
9	667.4	73.6	669	12	BT008160	BT008160
10	651.4	71.8	666	9	AY353086	AY353086
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ACCESSION	AX391276	Sequence 19 from Patent WO0073445.				
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ORGANISM						
REFERENCE						
AUTHORS						
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Ferrara, N., Williams, P.M., Baker, K.P., Ashkenazi, A.J., C						
Godowski, P.J., Gurney, A.L., Kuo, S.S., Mark, M.R., Marster						
Pitti, R.M., Wood, W.I., Gerber, H., Gerritsen, M.E., Paoni,						

anabe, C.K.
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VERSION AX697111.1 GI:29498075
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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AUTHORS Ferrera, N., Stewart, T.A., Williams, P.M., Baker, K.P., De
Raton, D.L., Gao, W.Q., Pan, J., Botstein, D., Fong, S., Goc
Godowski, P.J., Gurney, A.L., Smith, V., Tumas, D., Wood, W.
Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A. and We
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; Secreted Protein Discovery Initiative (SPDI), a Large-Scale
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; oinformatcs Assessment
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eration and initial analysis of more than 15,000 full-length
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c. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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tact: MGC help desk
il: cgapbs-re@mail.nih.gov
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milarity 73.8%; Score 669; DB 9; Length 669;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 503 AATGACAGGCGAGCTCTCTAAAGCGGAGATAAACCTCTACTTGCAGAGGAATT
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Db 601 AATGACATGATGCTGATGCTTCTCTTCTCCCAAGGAATACATGTATACCF
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QY 683 GAACATAG 691
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Db 661 GAACATAG 669
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RESULT 9
BT008160
LOCUS
DEFINITION Synthetic construct Homo sapiens FK506 binding protein
partial cds.
ACCESSION BT008160
VERSION BT008160.1 GI:30585158
KEYWORDS FLI CDNA.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 669)
AUTHORS Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Ei
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer
Phelan,M. and Farmer,A.
TITLE Cloning of human full-length CDSs in BD Creator(TM) Sys
vector
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 669)
AUTHORS Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Ei
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer
Phelan,M. and Farmer,A.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 E
Circle, Palo Alto, CA 94303, USA
COMMENT This CDS clone is a part of a collection of human full
expression clones generated by BD Biosciences Clontech
Harvard Institute of Proteomics. Each CDS has been clon
forms: with and without stop-codon (to allow fusion wit
tag). The CDS has been directionally cloned using BD I
cloning system between the Sali and HindIII sites of t
vector. Additional sequences in the clone: 'ACC' after
and before 'ATG' to provide Kozak consensus sequence;
last codon and before HindIII site to maintain reading
Clone distribution: http://bioinfo.clontech.com/orfclon
Location/Qualifiers
1. .669
/organism="synthetic construct"
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/clone="GH00727U1.0"
/clone_lib="BD Creator(TM) CDS Library derived

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Accession	Length	Library	Strain
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			PRI 27-AUG-2003

DEFINITION	Homo sapiens FK506-binding protein 7 (FKBP7) mRNA, complete cds			
ACCESSION	AY353086			
VERSION	AY353086.1 GI:34099838			
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut: Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo			
REFERENCE	1. (bases 1 to 666)			
AUTHORS	Li, H., Zhong, G., Yu, R., Shen, C., Zhou, G., Li, M., Xiao, W. and Yang, S.			
TITLE	Direct Submission			
JOURNAL	Submitted (29-JUL-2003) Guangzhou FuluGen Co., Ltd., 5 Guangzhou Entrepreneur Park for Overseas Chinese Scholars Rd., GERTD, Guangzhou, Guangdong 510730, China			
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Db	1	ATGCCAAAAACCATGATTTCTTATTTCAGATTCATTGTTTCTTTTATCTGTG		
Qy	83	TTTACTGCTCAGAGACAAAGAGAGAGAGACCGAAGAGTGAAAAATAGA		
Db	61	TTTACTGCTCAGAGACAAAAAGAGAGAGAGACCGAAGAGTGAAAAATAGA		
Qy	143	CATCGTCCGAAACTGCTCTTAAGACAAGCAAGAGGAGACCTTACTTAAATGC		
Db	121	CATCGTCCGAAACTGCTCTTAAGACAAGCAAGAGGAGACCTTACTTAAATGC		
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Db	241	CACCCCAATGGTTTGTTCCTTGTGTGGCAAGTCATAAAGGCCTTAGACAT		
Qy	323	ACAGATATGTGCCCTGGAGAAAACGAAAAAGTAGTTATACCCCTTCATTTCG		
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Qy	383	AAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTGA		
Db	361	AAGGAAGGCTAT--GAAGCAAGATTCACCCGATGCTACATTGATTTTGA		
Qy	443	CTTTATGCTGTGACCAAGGACCGAGCATTTAGACATTTTAAACAAATAGA		

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HAACATAG 691

HAACATAG 666

36754 761 bp DNA linear PAT 18-SEP-2002
 an protein having transmembrane domain and DNA encoding the

36754

36754.1 GI:23231699

2002506615-A/8.

o sapiens (human)

o sapiens

aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 malia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

o.S., Sekine,S., Kimura,T. and Nakamura,N.

an protein having transmembrane domain and DNA encoding the same

ent: JP 2002506615-A 8 05-MAR-2002;

AMI CHEMICAL RESEARCH CENTER, PROTEGENE INC

Homo sapiens (human)

JP 2002506615-A/8

25-FEB-1999 JP 2000533542

SEISHI KATO, SHINGO SEKINE, TOMOKO KIMURA, NOBUKO NAKAMURA PC

IN15/09,C07K14/705,C12N1/15,C12N1/19,C12N1/21,C12N5/10// PC

IP21/02,

C12N15/00,C12N5/00

Human protein having transmembrane domain

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same

Key Location/Qualifiers

source

1..761 /organism='Homo sapiens (human)'

Location/Qualifiers

1..761

/organism='Homo sapiens'

/mol_type='genomic DNA'

/db_xref='taxon:9606'

61.6%; Score 559; DB 6; Length 761;

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AGAAGTGAATAAGAGTTTGTGATCGTCCAGAAAACGCTCTAAGACAAGCAAGCAAGGG 180

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 741 GTGAGGCTGTTTCCAAACTT 761

RESULT 12

AF040252

LOCUS

DEFINITION

AF040252

AF040252.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

AF040252 866 bp mRNA linear RO

Mus musculus FK506-binding protein (FKBP23) mRNA, comp

AF040252

AF040252.1 GI:2827254

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; M

1 (bases 1 to 866)

Nakamura,T., Yabe,D., Kanazawa,N., Tashiro,K., Sasayam

Honjo,T.

Molecular cloning, characterization, and chromosomal l

of FKBP23, a novel FK506-binding protein with Ca2+-bin

Genomics 54 (1), 89-98 (1998)

99026129

9806833

2 (bases 1 to 866)

Nakamura,T., Yabe,D., Kanazawa,N., Tashiro,K., Sasayam

Honjo,T.

Direct Submission

Submitted (29-DEC-1997) Center for Molecular Biology a

o University, Shogoin-Kawahara-cho, Sakyo-ku, Kyoto 606, Japan

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58.0%; Score 525.8; DB 10; Length 866;
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Conservative 0; Mismatches 161; Indels 6; Gaps 2;

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Qy 751 AGTCACATTTCTCCAAAGTGTATTGCTATTTTCCCTATGAGAGATATTTT
Db 752 TACCACGGTCTCTATGTTGTTGTTATACCTGTTTCTTTTCTTTTCTTTTCTTTT
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RESULT 14
BD136747
LOCUS
DEFINITION Human protein having transmembrane domain and DNA encod
same.
ACCESSION BD136747
VERSION BD136747.1 GI:23231692
KEYWORDS JP 2002506615-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
Kato,S., Sekine,S., Kimura,T. and Nakamura,N.
Human protein having transmembrane domain and DNA encod
Patent: JP 2002506615-A 1 05-MAR-2002;
SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
OS Homo sapiens (human)
PN JP 2002506615-A/1
PD 05-MAR-2002
PF 25-FEB-1999 JP 2000533542
PI SEISHI KATO, SHINGO SEKINE, TOMOKO KIMURA, NOBUKO NAI
C12N15/09,C07K14/705,C12N1/15,C12N1/19,C12N1/21,C12N5/
C12P21/02,
PC C12N15/00,C12N5/00
CC Human protein having transmembrane domain
and DNA encoding the
CC same
FH Key Location/Qualifiers
FT source Location/Qualifiers
1. .387
/organism="Homo sapiens"
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Matches 363; Conservative 0; Mismatches 3; Indels 0,
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Db 1 ATGCAATTCCTATTACGATTCATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
Qy 95 AGACAAAGAAAGAGGAGAGACCGGAGAGTGAATAAGAGTGTGCAATTC
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Search completed: April 9, 2004, 09:44:48
Job time : 3965 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

cleic search, using frame_plus_p2n model

April 9, 2004, 09:45:16 ; Search time 3751 Seconds
(without alignments)
2565.224 Million cell updates/sec

US-10-015-480a-180

1189
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BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

3470272 seqs, 21671516995 residues

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length: 0
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Maximum Match 100%
Listing first 45 summaries

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GenEmbl.*

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27: em.ste.*
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32: em.htg_other.*
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41: em.htgo_other.*

pred. No. is the number of results predicted by chance to have
score greater than or equal to the score of the result being
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1189	100.0	669	9	BT007122	BT007122
2	1189	100.0	669	12	BT008160	BT00816
3	1189	100.0	907	6	AX391276	AX391276
4	1189	100.0	907	6	AX697111	AX697111
5	1189	100.0	907	9	AY359015	AY359015
6	1189	100.0	911	9	BC009711	BC009711
7	1189	100.0	971	6	BD192938	BD192938
8	1176	98.9	968	6	BD193126	BD193126
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29	457	38.4	89669	9	HSJ340H11	AL109755
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nine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
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ect Submission
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cle, Palo Alto, CA 94303, USA
s CDS clone is a part of a collection of human full length
ression clones generated by BD Biosciences Clontech and the
ward Institute of Proteomics. Each CDS has been cloned in two
rms: with and without stop-codon (to allow fusion with C-terminal
ing system between the Sali and HindIII sites of the pDNR-DUAL
tor. Additional sequences in the clone: 'ACC' after Sali site
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1.89e.00 Matches: 222
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100.00% Indels: 0
9 Gaps: 0
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before 'ATG' to provide Kozak consensus sequence; 'GG' after c codon and before HindIII site to maintain reading frame.
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12 Gaps: 0

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DEFINITION Sequence 19 from Patent WO0073445.
ACCESSION AX391276
VERSION AX391276.1 GI:19699941
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hc

REFERENCE 1
AUTHORS Ferrara, N., Williams, P.M., Baker, K.P., Ashkenazi, A.J.,
Godowski, P.J., Gurney, A.L., Kuo, S.S., Mark, M.R., Marste
Pitti, R.M., Wood, W.I., Gerber, H., Gerritsen, M.E., Paoni
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 AUTHORS Clark,H.F.
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VERSION
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ORGANISM
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Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J.,
Butterfield,Y.S., Krzyzanski,M.I., Skalska,U., Smalius,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (200
22388257
12477932
Strausberg,R.
Direct Submission
Submitted (29-JUN-2001) National Institutes of Health,
Gene Collection (MGC), Cancer Genomics Office, National
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Sequencing Group at the Stanford Hum
Center, Stanford University School of Medicine, Stanfor
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A.,
R. M.
Clone distribution: MGC clone distribution information
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A0IN37/18,A0IN43/04,C12Q1/00,C12Q1/02,C12Q1/69,C12N5/00 PC
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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BD193126.1 GI:33002865
JP 2002516573-A/220.
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artificial sequences.
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Young,P., Greene,H.S., Ferrie,A.M., Ruben,S.M., Rosen,C.
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Florence,C., Florence,K., Lafleur,D.W., Ni,J., Pan,P.,
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207 human secreted proteins
Patent: JP 2002516573-A 220 04-JUN-2002;
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PR 06-JUN-1998 US 60/048915, 06-JUN-1997 US 60/0
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18-DEC-1997 US 60/070923
PI PAUL YOUNG, JOHN M GREENE, ANN M FERRIE, STEVEN M RUB
PI ROSEN,
PI JING SHAN HU, HENRIK S OLSEN, REINHARD EBNER, LAURIE
PI PAUL A MOORE,
PI YANGGU SHI, CHARLES FLORENCE, KIMBERLY FLORENCE, DAVI
PI JIAN NI,
PI PING PAN, YING FEI WEI, CARRIE L FISCHER, DANIEL R SO
PI ZHIZHEN ZENG,
PI HUA KYAW, GUO LIANG YU, PING FENG, PATRICK J DILLON, G
ENDRESS,

KENNETH C CARTER
 A01N37/18.A01N43/04.C12Q1/00.C12Q1/02.C12Q1/68.C12N5/00 PC
 2N5/06.C12N15/00
 C12N15/06.C12N15/09.C12N15/10.C12N15/11.G01N33/53 CC
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 AY353086
 VERSION
 AY353086.1 GI:34099838
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
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 Li,H., Zhong,G., Yu,R., Shen,C., Zhou,G., Li,M., Xiao,Y
 and Yang,S.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (29-JUL-2003) Guangzhou FulengGen Co., Ltd.,
 Guangzhou Entrepreneur Park for Overseas Chinese Schol
 BaoShi Rd., GETDD, Guangzhou, Guangdong 510730, China
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 00751.1 GI:5410287
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 n, Z., Zhang, Q., Dai, M., Song, H., Wu, X., Mao, M., Fu, G.,
 M., Chen, J. and Hu, R.
 an FK506-binding Protein (FKBP23)-isoform gene
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 (bases 1 to 1067)

Received 23-October 1998; accepted 23-October 1998. Address correspondence to: Dr. J. H. Wu, Department of Molecular Medicine, Rui-Jin Hospital, Shanghai Institute of Molecular Medicine, 197, Rui-Jin Road II, Shanghai, P.R. China, 200025.

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 ORGANISM Mus musculus

RESULT 11

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DEFINITION

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3
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ACCESSION
NUMBER

VERSION
KEYWORDS

KEYWORDS
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SOURCE ORGANIS

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 uration and initial analysis of more than 15,000 full-length
 an and mouse cDNA sequences
 ac. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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il: cgapbs-remail.nih.gov
 ssue Procurement: Marcello Bento Soares, Ph.D.
 NA Library Preparation: M. Bento Soares, University of Iowa
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 a Sequencing by: Institute for Systems Biology
 p://www.systemsbioology.org

il: amadane@systemsbioology.org
 p Madan, Jessica Fahney, Erin Helton, Mark Kettelman, Anuradha
 an, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

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ure 159..452
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misc_feature /db_xref="CDD:pfam00254"
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ORIGIN

Alignment Scores:
 Pred. No.: 1.49e-97 Length: 863
 Score: 1013.00 Matches: 190
 Percent Similarity: 91.74% Conservative: 10
 Best Local Similarity: 87.16% Mismatches: 18
 Query Match: 15.20% Indels: 0
 DB: 10 Gaps: 0

US-10-015-480A-180 (1-222) x BC032961 (1-863)

Qy 5 MethHisPheLeuPheArgPheIleValPhePheTyrLeuTyrGlyLeuPheTl
 Db 42 ATGAATCTCTATTACAGACTAGCAGTTTCTTACCTGTGTTGTTGTCGG;
 Qy 25 ArgGlnLysLysGluGluSerThrGluGluValLysIleGluValLeuHisA
 Db 102 GGACAAACAAAGAAAGAACGACCTGAGGAAGTGAATAGAGTTTTCACCC
 Qy 45 AsnCysSerLysThrSerLysLysGlyAspLeuLeuAenAlaHisTyrAspG
 Db 162 AACTGCTCCAAAACAAGCAGGAAGAGACTTGTAAATGCCCATTAAGATG
 Qy 65 AlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGlyHisP
 Db 222 GCTAAAGACGCTCCAAATTTCTACTGACCGGACACAGATGAGGCCACC
 Qy 85 PheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMetThrA
 Db 282 TTGTGTTCTGTGTCGGACATGTCATAAAGGGGGCTGGACATTGCTATGATGG
 Qy 105 ProGlyGluLysArgLysValValIleProSerPheAlaTyrGlyLysG
 Db 342 CCTGGGAAAAGAGAAAGGTGATTATACCGCTTCGTTTGCATATGGAAAAG
 Qy 125 AlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGluLeuT
 Db 402 GCAGAAGCAAGATTCCACCAATGCAACTCTGATGTTTGAGATTGAACCTT
 Qy 145 ThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAspAsnA
 Db 462 ACCAAGACCAAGAGCATTGAAACATTTAAGCAATAGACACGATAATG
 Qy 165 LeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLysAspG
 Db 522 CTCTCCAAAGCTGAGATAGAGCTTTACTTACAGAAAGGACTTTGAAAAAGATG
 Qy 185 ArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLysAsnA
 Db 582 CGTGACAAAGTCATATACAGAGCGAGTTTGGAAAGATATCTTTAGAAAAATG
 Qy 205 GlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAspGluL
 Db 642 GGAGAGCGCTTCATTCTCTCTAGGAATACAAATGTGCACCAACATGATGAGC

RESULT 12
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 LOCUS Mus musculus FK506-binding protein (FKBP23) mRNA, comp.
 DEFINITION AF040252
 ACCESSION AF040252.1 GI:2827254
 VERSION
 KEYWORDS Mus musculus (house mouse)
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; M
 1 (bases 1 to 866)
 Nakamura,T., Yabe,D., Kanazawa,N., Tashiro,K., Sasayam
 REFERENCE
 AUTHORS

D	b		417	GCAGAGGCAAGATGCCACCANTGCAACTCTCTGATGTTCGAGATTGAACCTTTT
Q	y		145	ThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAspAsnAs
D	b		477	ACCAAAGGACCAAGGAGCATTGAAACATTTAAGCAATAAGACACCGGATAATGA
Q	y		165	LeuSerIlyAlaGluIleAsnLeuTyLeuGlnArgGluPheGluLysAspGI
D	b		537	CTCTCCAAAGCTGAGATAGAGCTTTTACTTACAGAAGGAGCTTTGAAAAAGATGC
Q	y		185	AtcAspLysSerTyrrGlnAspAlaValLeuGluAspIlePheLysLysAsnAs
D	b		597	CGTGACAAGTCATATCAGAAGGCGAGTTTTGGAGAATATCTTTAAGAAAAATGA
Q	y		205	GlyAspGlyPheIleSerProLysGluTyrrAsnValTyrrGlnHisAspGluLe
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R	E	S	ULT 13	
L	O	C	BD136754	
D	E	F		Human protein having transmembrane domain and DNA encoded same.
A	C	C	BD136754	
V	E	N	BD136754.1	GI:232321699
K	E	Y	JP	2002506615-A/8.
S	O	R	Homo sapiens	(human)
O	R	G	Homo sapiens	
R	E	F	Eukaryota; Metazoa;	Chordata; Vertebrata; Eut
R	E	F	Mammalia; Eutheria;	Primates; Catarrhini; Homiidae; Ho
A	T	H	1 (bases 1 to 761)	
A	T	H	Kato,S., Sekine,S., Kimura,T. and Nakamura,N.	
T	I	T	Human protein having transmembrane domain and DNA encoded	
J	O	N	Patent: JP 2002506615-A 8 05-MAR-2002;	
			SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC	
C	O	M	OS	Homo sapiens (human)
			PN	JP 2002506615-A/8
			PF	25-FEB-1999 JP 2000533542
			PI	SEISHI KATO,SHINGO SEKINE,TOMOKO KIMURA,NORUKO NAK
			C12N15/09,C07K14/705,C12N1/15,C12N1/19,C12N1/21,C12N5/1/	
			C12P21/02,	
			PC	C12N15/00,C12N5/00
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			and DNA encoding the	
			CC	same
			PH	Key
			FT	source
			Location/Qualifiers	
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			Matches:	176
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 HisProLysTyrPheValLeuGlyValGlnValIleLysGlyLeuAspIleAlaMet 100
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 LysGluGlyTyr-AlaGluGlyLysIleProAspAlaThrLeuIlePheGluIleG1 140
 AAGGAAGGCTATGATA----- 433
 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAs 160
 ----- 433
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 malia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 (bases 1 to 387)
 o.S., Sekine.S., Kimura.T. and Nakamura.N.
 nan protein having transmembrane domain and DNA encoding the same
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 JAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
 Homo sapiens (human)
 JP 2002506615-A/1
 05-MAR-2002
 25-FEB-1999 JP 2000533542
 SSISHI KATO,SHINGO SEKINE,TOMOKO KIMURA,NOBUKO NAKAMURA PC
 2N15/09,C07K14/705,C12N1/15,C12N1/19,C12N1/21,C12N5/10// PC
 2P21/02.
 C12N15/00,C12N5/00
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 Location/Qualifiers

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 Query Match: 54.92% Gaps: 0
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 Db 1 ATGCATTTCCTATTTCAGATTTCATTCTTTTCTTTTATCTGTGGGCCCTTTTFA
 Qy 25 ArgGlnLysLysGluGluSerThrGluGluValLysIleGluValLeuHisAla
 Db 61 AGACAAAGAAAGAGAGAGACCCAGAGAGTGAATAGAGTTTGCATC
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 Db 121 AACCTGCTTAAGCAAGCAAGAGAGGAGACCTACTAAATGCCATTATGACG
 Qy 65 AlalysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGlyHisP
 Db 181 GCTAAAGACGGCTCGAAATTCCTACTGCGCGGACACAAATGAAGGCCACC
 Qy 85 PheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMetThrA
 Db 241 TTTGTTCTTGGTGTGGCAAGTCATAAAGGCCCTAGACATTGCTATGACAG
 Qy 105 ProGlyGluLysArgLysValValIleProProSerPheAlaTyrGlyLysG
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 LOCUS
 DEFINITION Mus musculus cDNA sequence BC029109, mRNA (cDNA clone 1
 IMAGE:3985764), complete cds.
 ACCESSION BC029109
 VERSION BC029109.1 GI:22137712
 KEYWORDS MGC.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
 Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; M
 1 (bases 1 to 2714)
 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M.,
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F.,
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J.,
 Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., H
 Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.
 Scheetz,T.E., Brownstein,M.J., Uadin,T.B., Toshiyuki,S
 Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Pei
 Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
 McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.
 Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W
 Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibb
 Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,
 Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchen
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J.,
 Butterfield,Y.S., Krzywinaki,M.I., Skalska,U., Smailus
 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 fu
 human and mouse cDNA sequences
 TITLE

6.52e-46	Length:	2714
529.50	Matches:	105
65.91%	Conservative:	40
47.73%	Mismatches:	64
44.53%	Indels:	11
10	Gaps:	4

Search completed: April 9, 2004, 11:57:53
Job time : 3769 secs

180 (1-222) x BC029109 (1-2714)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using frame_plus_p2n model

April 9, 2004, 08:38:41 ; Search time 416 Seconds
(without alignments)
2267.067 Million cell updates/sec

US-10-015-480A-180

1189
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

3373863 seqs, 2124099041 residues

hits satisfying chosen parameters: 6747726

length: 0
length: 2000000000

: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: Geneseqn2003cs:.*
10: Geneseqn2004s:.*

is the number of results predicted by chance to have a
ater than or equal to the score of the result being printed,
rived by analysis of the total score distribution.

SUMMARIES

Query Match	Length	DB ID	Description
100.0	907	3 AAA77672	Aaa77672 Human PRO
100.0	907	3 AAA37073	Aaa37073 Human PRO
100.0	907	4 AAF54329	Aaf54329 DNA encod
100.0	907	4 AAC90572	Aac90572 Human PRO
100.0	907	8 ACD68366	Acd68366 Novel hum
100.0	907	8 ACD04468	Acd04468 Human cdn
100.0	907	8 ACD68012	Acd68012 Novel hum
100.0	907	9 ADC18048	Adc18048 Human PRO

	9	1189	100.0	907	9	ADD70694
10	1189	100.0	907	9	ADD39771	Add70694
11	1189	100.0	907	9	ADD70217	Add70217
12	1189	100.0	907	9	ADD38338	Add38338
13	1189	100.0	907	9	ADD39294	Add39294
14	1189	100.0	907	9	ADD38817	Add38817
15	1189	100.0	907	9	ADD40248	Add40248
16	1189	100.0	907	9	ADBS0469	Ades0469
17	1189	100.0	907	9	ADBS20081	Ades20081
18	1189	100.0	907	9	ADBS4992	Ades4992
19	1189	100.0	907	9	ADBS21550	Ades21550
20	1189	100.0	931	7	ADA40140	Ada40140
21	1189	100.0	931	7	ADC73702	Adc73702
22	1189	100.0	971	2	AAV84433	Avv84433
23	1189	100.0	971	4	ABA83216	Aba83216
24	1189	100.0	971	7	ADA40497	Ada40497
25	1189	100.0	971	8	ACH04717	Ach04717
26	1189	100.0	971	8	ACD44527	Acd44527
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29	1176	98.9	968	2	AAV84621	Avv84621
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31	1176	98.9	968	7	ADA40498	Ada40498
32	1176	98.9	968	8	ACH04906	Ach04906
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34	1176	98.9	968	9	ADC73948	Adc73948
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36	859.5	72.3	843	9	ADBS79053	Ades79053
37	838	70.5	600	3	AAA44235	Aaa44235
38	675.5	56.8	493	8	ACH33348	Ach33348
39	653	54.9	387	2	AAZ11176	Aaz11176
40	524	44.1	633	2	AAZ22201	Aaz22201
41	524	44.1	633	8	ACD40527	Acd40527
42	524	44.1	1623	7	ADA40062	Ada40062
43	524	44.1	1623	9	ADC73647	Adc73647
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ALIGNMENTS

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AC AAA77672;
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DT 07-NOV-2000 (first entry)
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XX cytostatic; gene therapy; vaccine; ss.
XX
OS Homo sapiens.
XX
XX WO200032221-A2.
PN
XX
XX 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US028313.
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XX 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 12-JAN-1999; 99US-0115554P.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.

9; 99US-0144758P.
9; 99US-0145698P.
9; 99WO-US020111.
9; 99WO-US020594.
9; 99WO-US020944.
9; 99WO-US021090.
9; 99WO-US021547.
9; 99WO-US023089.
9; 99US-0162506P.

NENTECH INC.

AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
Watanabe CK, Williams PM, Wood WI;

412154/35.
AB24429.

ids encoding PRO polypeptides useful for preventing, diagnosing
ing diagnosing a cardiovascular, endothelial or angiogenic
in mammals.

Fig 83; 315pp; English.

it invention describes nucleic acids encoding PRO polypeptides
; preventing, diagnosing and treating diagnosing a
ular, endothelial or angiogenic disorder in mammals by
f cell proliferation, angiogenesis and cardiovascularisation,
identifying agonists and antagonists of these processes. The
ids and the proteins they encode may be used in the prevention,
and diagnosis of diseases associated with inappropriate PRO
i such as cardiovascular, endothelial or angiogenic disorders in
g, atherosclerosis, cancers and cardiac hypertrophy). For
he nucleic acids (NCs) and vectors containing them and the PRO
he may be used to treat disorders associated with decreased PRO
1. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
and protein sequences used in the exemplification of the
vention

307 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;

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2.87e-129 Length: 907
1189.00 Matches: 222
city: 100.00% Conservative: 0
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100.00% Indels: 0
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HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
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Qy 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleA
Db 443 CTTATGCTGTGACCAAGGACCGAGCATTTTAAACAAATAG
Qy 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluP
Db 503 AATGACAGGCGCTCTCTAAAGCGGAGATAACCTCTACTTGCAGAGGAAT
Qy 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIleP
Db 563 GATGAGAGGCGACGTGACAGTCTATATCAGATGCAGTTTGTAGAGATATT
Qy 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrG
Db 623 AATGACCATGATGCTGATGCTTCATTTCCTCCCAAGGATACATATGATACCI
Qy 221 GluLeu 222
Db 683 GAACATA 688
RESULT 2
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XX 08-AUG-2000 (first entry)
DT Human PRO1304 (UNQ670) cDNA sequence SEQ ID NO:179.
XX Human; PRO polypeptide; membrane bound protein; receptor; dia
KW transmembrane; secretion; immunoadhesion; pharmaceutical; scr
XX Homo sapiens.
XX WO200012708-A2.
XX 09-MAR-2000.
PF 01-SEP-1999; 99WO-US020111.
XX 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
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PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.

98US-0100662P.
 98US-0100664P.
 98US-0100683P.
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 98US-0100710P.
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 98US-0103449P.
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 98US-0104987P.
 98US-0105000P.
 98US-0105002P.
 98US-0105104P.
 98US-0105169P.
 98US-0105266P.
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 98US-0105694P.
 98US-0105807P.
 98US-0105881P.
 98US-0105882P.
 98US-0106062P.
 98US-0106023P.
 98US-0106029P.
 98US-0106030P.
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 98US-0106033P.
 98US-0106178P.
 98US-0106248P.
 98US-0106384P.
 98US-0108500P.
 98US-0106464P.

03-NOV-1998; 98US-0106856P.
 03-NOV-1998; 98US-0106902P.
 03-NOV-1998; 98US-0106905P.
 03-NOV-1998; 98US-0106919P.
 03-NOV-1998; 98US-0106932P.
 03-NOV-1998; 98US-0106934P.
 10-NOV-1998; 98US-0107783P.
 17-NOV-1998; 98US-0108775P.
 17-NOV-1998; 98US-0108779P.
 17-NOV-1998; 98US-0108787P.
 17-NOV-1998; 98US-0108788P.
 17-NOV-1998; 98US-0108801P.
 17-NOV-1998; 98US-0108802P.
 17-NOV-1998; 98US-0108806P.
 17-NOV-1998; 98US-0108807P.
 17-NOV-1998; 98US-0108867P.
 17-NOV-1998; 98US-0108925P.
 18-NOV-1998; 98US-0108848P.
 18-NOV-1998; 98US-0108849P.
 18-NOV-1998; 98US-0108850P.
 18-NOV-1998; 98US-0108851P.
 18-NOV-1998; 98US-0108852P.
 18-NOV-1998; 98US-0108858P.
 18-NOV-1998; 98US-0108904P.
 (GETH) GENENTECH INC.
 Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood
 WPI; 2000-237871//20.
 P-PSDB; AAY99391.
 New mammalian DNA sequences encoding transmembrane, receptor or
 PRO polypeptides, useful for screening of potential peptide or
 molecule inhibitors of the relevant receptor/ligand interaction
 Claim 2; Fig 103; 773pp; English.
 AAA37022 to AAA37144 encode the new isolated human transmembral
 receptor or secreted PRO polypeptides given in AAY99340 to AAY:
 transmembrane and receptor PRO proteins can be used for screen:
 potential peptide or small molecule inhibitors of the relevant
 receptor/ligand interactions. The polypeptides and nucleotide
 encoding then have various industrial applications, including
 pharmaceutical and diagnostic agents. AAA37145 to AAA37330 rep:
 primers and hybridisation probes used in the isolation of the
 polypeptides from the present invention
 SQ Sequence 907 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: Length: 2.87e-129 907
 Score: 1189.00 Matches: 222
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0
 US-10-015-480A-180 (1-222) x AAA37073 (1-907)
 QY 1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTyr
 DB 23 ATGCCAAAACCATGCATTTCTTATT CAGATTCA TTGTTTCTTTATCTGCG
 QY 21 PheThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleGlu
 DB 83 TTTACTGCTCAGACAAAAGAAAGAGAGAGACCCGAGAGAGTGAANAATAG
 QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAla
 DB 143 CATCGTCCAGAAAAC TCTCTTAAGACCAAGCAAGGAGGAGACCTACTAAATGSC
 QY 61 AspGlyTyrLeuAlaLysAspLysSerLysPheTyrCysSerArgThrGlnAsr

|||||TACCTGGCTAAGACGGCTCGAAATTCCTACTGCGACCGGACACAAAATGAAGGC 262
 isProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMet 100
 ACCCCAAATGGTGTGTTCTGGTGGTGGCAAGTCATATAAAGCCCTAGACATTGCTATG 322
 hrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAlaTyrGly 120
 CAGATATGTCCTCGAGAAAGCGAAAGTAGTTATACCCCTTCATTGTGATACGGA 382
 ysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
 AGAAGGCTATGCAGAAAGCAGATTCCACCGGATGCTACATTGATTTTGAGATTCAA 442
 euTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
 TTTATGCTGTGACCAAGACCCGCGAGCATTTGAAGCATTTAAACAAATAGACATGGAC 502
 snAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
 ATGACAGGCGAGCTCTCTAAGCCGAGATTAACCTCTACTTGCAAGGGAATTTGAAAA 562
 spGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
 ATGAGAAGCCACCGTACCAAGTCATATCAGGATGCAAGTTTGAAGATATTTTAAAGAAG 622
 snAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAsp 220
 ATGACCATGATGTGTGATGGCTTCATTCTCCCAAGGAATACAAATGATATACCAACGAT 682

l:Leu 222

:AACTA 688

standard; DNA; 907 BP.

1 (first entry)

ng protein of the invention #52.

transmembrane; gene therapy; ss.

ed.

1-A1.

10.

10; 2000WO-US004342.

19; 99US-0141037P.

19; 99US-0144758P.

19; 99US-0145698P.

19; 99WO-US020111.

19; 99US-0182506P.

19; 99WO-US028313.

19; 99WO-US028551.

19; 99WO-US030095.

10; 2000WO-US000219.

10; 2000WO-US000376.

3NENTECH INC.

Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 ddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 oni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 N, Wood WI;

WPI; 2001-071395/08.

Secreted and transmembrane proteins and nucleic acids designat
 useful as hybridization probes, in chromosome and gene mapping
 therapy.

Claim 2; Fig 103; 787pp; English.

The present invention relates to secreted and transmembrane pr
 These proteins and the DNA encoding them may be used as hybrid
 probes, in chromosome and gene mapping and in the generation c
 sense RNA and DNA. They may also be used to generate eith
 transgenic animals or knockout animals which are in turn usefu
 development and screening of therapeutically useful reagents.
 acids may also be used in gene therapy

Sequence 907 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.87e-129 Length: 907
 Score: 1189.00 Matches: 222
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-015-480A-180 (1-222) x AAF54329 (1-907)

Qy 1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuT
 Db 23 ATCCCAAAACCATGCTATTCCTATTATTCAGATTCACTGTTCTTTTATCTGTC
 Qy 21 PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleG
 Db 83 TTACTGCTCAGAGACAAAGAAAGAGAGAGAGACCCGAGAGAGTGAATAAG
 Qy 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnA
 Db 143 CATCGTCCAGAAACCTCTTAAGACAAGCAAGCAAGAGGAGACCTACTAAATG
 Qy 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnA
 Db 203 GACGGGTACCTGGCTAAAGACGGCTCGAAATTCCTACTGACGCGGACACAA
 Qy 81 HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspI
 Db 263 CACCCCAATGGTGTGTTCTTGTGTGGCAAGTCATATAAAGGCGCTAGACA
 Qy 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheA
 Db 323 ACAGATATGTCCCTCGAGAAAGCGAAAGTAGTTATATACCCCTTCATTTG
 Qy 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheG
 Db 383 AAGGAGGCTATGCAGAAAGCAAGATTCCACCGGATGCTACATTGATTTTGT
 Qy 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleA
 Db 443 CTTTATGCTGTGACCAAGGACCCAGGAGCATTTAGACATTTAAACAAATAG
 Qy 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluP
 Db 503 AATGACAGGCGAGCTCTCTAAAGCGGAGATAAACCTCTACTTGAAGGGAAT
 Qy 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIleP
 Db 563 GATGAGAGGACGCTGCAAGTCATATCAGGATGCGAGTTTGAAGATATTT
 Qy 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrG
 Db 623 AATGACCATGATGGTGTGATGGCTTCATTTCTCCCAAGGAATACATGATACCI
 Qy 221 GluLeu 222

||||
ACTA 688

andard; cDNA; 907 BP.

(first entry)

04 cDNA.

cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;
antiathermatic; antiarthritic; antiinflammatory; cytostatic;
antianalger; gene therapy; cardiovascular disease;
disorder; angiogenic disorder; cancer; periodontal disease;
ng; ss.

is.

-A2.

1.

1; 2000WO-US013705.

1; 99WO-US012252.

1; 99US-0141037P.

1; 99US-0144758P.

1; 99US-0145698P.

1; 99US-0146222P.

1; 99WO-US020111.

1; 99WO-US028313.

1; 99WO-US028409.

1; 99WO-US028565.

1; 99WO-US030095.

1; 2000WO-US000219.

1; 2000WO-US000376.

1; 2000WO-US003565.

1; 2000WO-US004341.

1; 2000WO-US004342.

1; 2000WO-US005004.

1; 2000WO-US005841.

1; 2000WO-US006319.

1; 2000WO-US006884.

1; 2000WO-US007532.

1; 2000WO-US008439.

TECH INC.

W, Baker KP, Ferrara N, Gerber H, Gerritsen ME;

Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;

Pitti RM, Watanabe CK, Williams PM, Wood WI;

125251/03.

150960.

nucleic acids encoding PRO polypeptides which are useful in
and treatment of cardiovascular, endothelial or angiogenic
in a mammal.

Fig 19; 182pp; English.

sequence is one of seventeen nucleic acids encoding PRO
as. The PRO nucleic acids, polypeptides, agonists and
are useful for treating cardiovascular, endothelial or
disorders in a mammal. Examples of these disorders include
atrophy, trauma, cancer, age-related macular degeneration,
rosis, hypertension, arterial restenosis, Reynaud's disease,
arthritis, angina, myocardial infarctions, thrombophlebitis
ginitis. The PRO polypeptides and antagonists are also used to
hour angiogenesis and for treating periodontal diseases. They

CC are also used to stimulate wound healing and tissue regenerati
CC nucleic acids, polypeptides and anti-PRO antibodies are useful
CC diagnosing a cardiovascular, endothelial or angiogenic disorder
XX
SQ Sequence 907 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.87e-129	Length:	907
Score:	1189.00	Matches:	222
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-015-480A-180 (1-222) x AAC90572 (1-907)

QY	1	MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTr
DB	23	ATGCCAAAACCATGCTTCTTATTCAGATTCTTTTCTTTTATCTGTG
QY	21	PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGln
DB	83	TTTACTGCTCAGACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
QY	41	HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAl
DB	143	CATCGTCCAGAAACTGCTCTAAGACAAGCAAGAGAGAGAGAGAGAGAGAGAG
QY	61	AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsi
DB	203	GACGGCTACCTGGCTAAAGACGGCTCGAAATTTCTACTGCAGCCGACACAAA
QY	81	HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIle
DB	263	CACCCCAATGGTTTGTCTTGGTGTGGCAAGTCATAAAAGGCGCTAGACAT
QY	101	ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAl
DB	323	ACAGATATGTGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
QY	121	LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGln
DB	383	AAGGAAGGCTATGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
QY	141	LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs
DB	443	CTTTATGCTGTGACCAAGGACACGAGAGAGAGAGAGAGAGAGAGAGAGAG
QY	161	AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPh
DB	503	AATGACAGGCGAGCTCTCTAAAGCCGAGATAAAACCTCTACTTGCAGAGGAAT
QY	181	AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePh
DB	563	GATGAG
QY	201	AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGln
DB	623	AATGACCATGATGGTGTGAGGCTTCTATTTCTCCCAAGGAATACAAATGTATACCA
QY	221	GluLeu 222
DB	683	GAACATA 688

RESULT 5

ACD68366

ID ACD68366 standard; cDNA; 907 BP.

XX ACD68366;

XX 17-SEP-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO1304 cDNA.

reted and transmembrane protein; PRO; angiogenesis;
es cell proliferation; wound healing; immune response;
es proliferation; neonatal heart hypertrophy; tumour;
sufficiency disorder; calcium flux; inflammation;
ndothelial growth factor-stimulated proliferation;
kidney mesangial cell proliferation; Berger disease;
y; Schanlein-Henoch purpura; celiac disease; Crohn's disease;
herpetiformis; diabetes; haemoglobin switch; insulinemia;
beta-cell precursor cell differentiation; thalassemias;
udatory hair cell regeneration; hearing loss; bone disorder;
disorder; sports injury; arthritis; gene; ss.

52

30-A1.

3

1; 2001US-00015869.

8; 98US-0098716P.

8; 98US-0098749P.

8: 98US-0098803P.

8; 98US-0098843P.

8; 98US-0099596P.

98US-0099602P.

8; 98US-0099741P.

8; 98US-0099763P;

8; 98US-0099808P.

8; 98US-0099815P.

98US-0100385P.

8; 98US-0100390P.

3; 98US-0100627P.

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8; 98US-0101474P.

8; 98US-0101476P.

8; 98US-0101479P.

8; 98US-0101741P.

8; 98US-0101916P.

PR	29-SEP-1998	98US-1012240P
PR	29-SEP-1998	98US-1012307P
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PR	29-SEP-1998	98US-1012331P
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PR	30-SEP-1998	98US-1012487P
PR	30-SEP-1998	98US-1012570P
PR	30-SEP-1998	98US-1012571P
PR	01-OCT-1998	98US-1012684P
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PR	02-OCT-1998	98US-1012656P
PR	06-OCT-1998	98US-1013258P
PR	07-OCT-1998	98US-1013449P
PR	07-OCT-1998	98US-1013311P
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PR	07-OCT-1998	98US-1013401P
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PR	08-OCT-1998	98US-1013679P
PR	08-OCT-1998	98US-1013711P
PR	14-OCT-1998	98US-1014257P
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PR	20-OCT-1998	98US-1015000P
PR	20-OCT-1998	98US-1015104P
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PR	26-OCT-1998	98US-1015693P
PR	26-OCT-1998	98US-1015694P
PR	26-OCT-1998	98US-1015807P
PR	27-OCT-1998	98US-1015881P
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PR	30-OCT-1998	98US-1016464P
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PR	03-NOV-1998	98US-1016905P
PR	03-NOV-1998	98US-1016919P
PR	03-NOV-1998	98US-1016932P
PR	03-NOV-1998	98US-1016934P
PR	10-NOV-1998	98US-1017783P
PR	17-NOV-1998	98US-1018775P
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PR	18-NOV-1998	98US-1018849P
PR	18-NOV-1998	98US-1018849P
PR	18-NOV-1998	98US-1018850P
PR	18-NOV-1998	98US-1018851P
PR	18-NOV-1998	98US-1018852P
PR	18-NOV-1998	98US-1018858P
PR	18-NOV-1998	98US-1018904P
PR	22-DEC-1998	98US-1011423P
PR	30-DEC-1998	98US-1011423P
PR	30-DEC-1998	98US-1011423P
PR	05-JAN-1999	98US-1012010P

99WO-US000106.

99US-0129674P.
 99US-0141037P.
 99US-0144758P.
 99US-0145698P.
 99WO-US020111.
 99WO-US021194.
 99US-0162506P.
 99WO-US028313.
 99WO-US028551.
 99WO-US030095.
 2000WO-US0300219.
 2000WO-US0300376.
 2000WO-US0303565.
 2000WO-US004342.
 2000WO-US005004.
 2000WO-US005841.
 2000WO-US006884.
 2000WO-US013705.
 2000WO-US014042.
 2000WO-US014941.
 2000WO-US015264.
 2000WO-US023522.
 2000WO-US023328.
 2000WO-US030952.
 2000WO-US030873.
 2000WO-US032678.
 2001WO-US006520.
 2001WO-US006666.
 2001WO-US017800.
 2001WO-US019692.
 2001WO-US021066.
 2001WO-US021735.
 2001US-00946374.

ENTECH INC.

Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 dard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 ni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 Wood WI;

85293/55.

33633.

ted PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
 t modulate glucose or free fatty acid uptake by skeletal
 s, and are useful for treating diabetes, hyper- or hypo-

:	2.87e-129	Length:	907
	1189.00	Matches:	222
ty:	100.00%	Conservative:	0
arity:	100.00%	Mismatches:	0
	100.00%	Indels:	0
	8	Gaps:	0

80 (1-222) x ACD68366 (1-907)

tProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTyrGlyLeu 20
 GC AAAAACCATGATCTTATTCAGATTCAATGTTTCTTTTATCTGTGGGCGCTT 82
 eThrAlaGlnArgGlnLysGluGluSerThrGluGluValLysIleGluValLeu 40
 TACTGCTCAGACAAAGAAAGAGGAGACCCGAGAGAGTGAAGTAAATAGAGTTTG 142
 sArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
 TCGTCCAGAAAACTGCTCTAAGACAGCAAGAGAGGAGACCTACTTAATGCCATTAT 202
 pGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
 CGGCTACCTGGCTAAAGACGGCTCGAAATTCCTACTGCGCGGACACAAATGAAGGC 262

Qy	81	HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIle
Db	263	CACCCCAATGTTTGTCTTGGTGTGGCAAGTCATAAAGCGCTAGACATT
Qy	101	ThrAspMetCysProGlyGluLysArgLysValIleProProSerPheAla
Db	323	ACAGATATGTCCTGGAGAAAAGCGAAAGTAGTTATACCCCTTCATTTCG
Qy	121	LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGly
Db	383	AAGGAGCGCTATGCAGAAAGCAAGATTCCACCGGATGCTCATTTGATTTTGAC
Qy	141	LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAsi
Db	443	CTTTATGCTGTGACCAAGGACCAAGGAGCATTCAGACATTTAACAATAGAC
Qy	161	AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPhe
Db	503	AATGACAGGCGAGCTCTCTAAAGCGGAGATAACCTCTACTTGCAGGGAATT
Qy	181	AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePhe
Db	563	GATGAGAAGCCACGTGACAGTCATATCAGGATGCAGTTTGTAGAGATATTTT
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RESULT 6
 ACH04468
 ID ACH04468 standard; cDNA; 907 BP.
 AC ACH04468;
 XX
 DT 01-OCT-2003 (first entry)
 XX
 DE Human cDNA encoding secreted/transmembrane protein PRO1304.
 XX
 KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
 KW cardiac; antidiabetic; anorectic; antiarthritic; angiogenesis;
 KW adrenal cortical capillary; endothelial cell growth; wound heal
 KW stimulated T-lymphocyte proliferation; immune response suppress
 KW neonatal heart hypertrophy; cardiac insufficiency disorder;
 KW vascular endothelial growth factor; inflammation; mononuclear
 KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insu
 KW chondrocyte redifferentiation; bone disorder; cartilage disorder
 KW sports injury; arthritis.
 OS Homo sapiens.
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 PN US2003044841-A1.
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 PD 06-MAR-2003.
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 PF 06-DEC-2001; 2001US-00006856.
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 PR 01-SEP-1998; 98US-0098716P.
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PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
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PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 03-JUL-2001; 2001WO-US021735.

2001US-00946374.

ENTECH INC.

Botstein D, Deenoyers L, Eaton DL, Ferrara N, Fong S, Gdard A, Godowski Fu, Grimaldi JC, Gurney AL, Hillan KJ, ni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI;

92259/46.

4486.

ted and transmembrane polypeptides and polynucleotides em useful for treating various cardiac insufficiency bone and/or cartilage disorders such as sports injuries and

2.87e-129 Length: 907
1189.00 Matches: 222
ty: 100.00% Conservative: 0
arity: 100.00% Mismatches: 0
100.00% Indels: 0
8 Gaps: 0

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eThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleGluValLeu 40
TACTGCTCAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 142
sArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
TCGTCAGAAAACCTGCTCTTAAGACACAGAGAGAGAGAGAGAGAGAGAGAGAG 202
pGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
CGGTACTCTGGCTAAAGACGGCTCGAAATTTCTAGCAGCGGACACAAATGAAGGC 262
sProLysThrPheValLeuGlyValGlyGlnValLysLysGlyLeuAspIleAlaMet 100
CCCCAAATGTTTGTCTTGTGTGTGGCAAGTCATAAAGCGCTAGACATTGCTATG 322
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AGATATGTCCTGGAGAAAGCGAAAGTAGTTATACCCCTTCATTTGCATACCGA 382
sGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
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TGACCATGATGTGTGGCTTCTTTCTCCAGGAGATACATGTATATACACACGAT 682
uLeu 222
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Db 683 GAACTA 688

RESULT 7

ACD68012

XX ACD68012 standard; cDNA; 907 BP.

XX AC ACD68012;

XX DT 17-SEP-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO1304 cDNA.

XX KW Human; secreted and transmembrane protein; PRO; gene therapy; tissue typing; chromosome identification; vaccine; gene; ss.

XX OS Homo sapiens.

XX FN US2003073129-A1.

XX PD 17-APR-2003.

XX PF 04-SEP-2001; 2001US-00946374.

XX PR 01-SEP-1998; 98US-0098716P.

XX PR 01-SEP-1998; 98US-0098723P.

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PR 22-DEC-1998; 98US-00218517.
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 PR 30-DEC-1998; 98US-0114223P.
 PR 05-JAN-1999; 99WO-US000106.
 PR 12-APR-1999; 99US-00284291.
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 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
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 PR 16-DEC-1999; 99WO-US030095.
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 PR 02-MAR-2000; 2000WO-US005841.
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 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001US-00872035.
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 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hi
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W
 PI Williams PM, Wood WI;
 XX WPI; 2003-585292/55.
 DR P-P8DB; ABO33510.
 XX
 PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, usef
 PT preparation of a medicament for treating a condition responsiv
 PT polypeptide, and as therapeutic agents e.g. vaccines.
 XX
 PS Claim 2; Fig 103; 561pp; English.
 XX
 CC The invention describes an isolated PRO (secreted and transmem
 CC polypeptide (I), having at least 80% sequence identity to a se

Alignment Scores:
 Pred. No.: 2,878-129 Length: 907
 Score: 1189.00 Matches: 222
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-015-480A-180 (1-222) x ACD68012 (1-907)

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uLeu 222

ACTA 688

andard; cDNA; 907 BP.

(first entry)

olynucleotide #52.

gene; ss; protein electrophoresis; chromosome mapping;
g; genetic disorder.

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PR 21-OCT-1998;

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 3: 2000WO-US000219.
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 3: 2000WO-US003565.
 3: 2000WO-US004342.
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 3: 2000WO-US014042.
 3: 2000WO-US014941.
 3: 2000WO-US015264.
 3: 2000WO-US023522.
 3: 2000WO-US023328.
 3: 2000WO-US030952.
 3: 2000WO-US030873.
 3: 2000WO-US032678.
 3: 2001WO-US006520.
 1: 2001WO-US006666.

PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hi
 PI Pan J, Paori NF, Roy MA, Smith V, Stewart TA, Tumas D, W
 PI Williams PM, Wood WI;
 XX WPI: 2003-555602/52.
 DR P-PSDB; ADC18049.
 XX
 PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, usef
 PT preparation of a medicament for treating a condition responsiv
 PT polypeptide, and as therapeutic agents e.g. vaccines.
 XX
 XX Claim 2; SEQ ID NO 179; 555pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynu
 CC encoding them. The sequences are useful in the preparation of
 CC medicament for treating a condition responsive to a PRO polype
 CC polypeptides are useful in a number of functional biological a
 CC molecular weight markers for protein electrophoresis and as th

Alignment Scores:
 Pred. No.: 2,87e-129 Length: 907
 Score: 1189.00 Matches: 222
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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US-10-015-480A-180 (1-222) x ADC18048 (1-907)

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 Db 23 ATGCCAAAACCATGCAATTCCTATTTCAGATTCATGTTTCTTTTATCTGIG
 QY 21 PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGI
 Db 83 TTTACTGCTCAGACAAAAGAAAGAGGAGAGCACCAGAAAGAGTGAATAAGA
 QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAl
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 QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAs
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 QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAl
 Db 323 ACAGATATGTGCCCTGGAGAAAAGCGAAAGTAGTTATACCCCTTCATTGTC
 QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGI
 Db 383 AAGGAGGCTATGCAGAGGCAAGATTCCACCGGATGCTACATTGATTTTTCG
 QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs
 Db 443 CTTTATGCTGTGACCAAGAGCACCAGGACATTGAGACATTTAAACAAATAGA
 QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPh
 Db 503 AATGACAGGCGCTCTCTTAAGCCGAGATAAAACCTCTACTTGCAAAGGGAATT

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 TGAGAAGCCACGTCACAAGTCATATCAGGATGCAGTTTGAAGATATTTTAAAGAAG 622

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uleu 222

|||||
ACTA 688

andard; cDNA; 907 BP.

(first entry)

encoding secreted/transmembrane protein PRO1304.

gene; secreted protein; transmembrane protein; PRO; tumour;
 onse; cardiac insufficiency disorder; calcium flux;
 ein endothelial cell; bone disorder; cartilage disorder;
 wound healing; diabetes; skeletal muscle cells; obesity;
 ase; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 herpetiformis; Crohn's disease; thalassaemia.

S.

5-A1.

2001US-00015386.

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 17-NOV-1998; 98US-0108779P.

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2.87e-129
1189.00
Length: 907
Matches: 222

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Qy	1 MetProLysThrWetHisPheLeuPheArgPheIleValPhePheTyrLeuTyr		
Db	23 ATCCGAAAAACCATGCAATTTCTTATTACAGATTCATTTCTTTTATCTGTG		
Qy	21 PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGlg		
Db	83 TTTTACTGCTCAGAGACAAAGAAAGAGAGAGACCCGAGAAGTGAATAAGA		
Qy	41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAl		
Db	143 CATCGTCCAGAAAACGTCTCTAAGACAAAGCAAGAGGAGACCTTACTAAATGC		
Qy	61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAs		
Db	203 GAGCGCTACTCGCTAAAGACGGCTCGAAATTTCTACTGCAGCCGGACACAAA		
Qy	81 HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIl		
Db	263 CACCCCAATGGTTTGTCTTGTGTGTGGCAAGTCATAAAAGGCTTAGACAT		
Qy	101 ThrAspWetCysProGlyGluLysArgLysValIleProProSerPheAl		
Db	323 ACAGATATGTGCCCTGGAGAAAACGCAAAAGTAGTTATACCCCTTCATTTCG		
Qy	121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGl		
Db	383 AAGGAAGCTATGCAGAGGCAAGATTCACCGGATGCTCAATTGATTTTGA		
Qy	141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs		
Db	443 CTTTATGCTGTGACCAGAGACCCAGAGCATTTGAGACATTTAAACAAATAGA		
Qy	161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPh		
Db	503 AATGACAGGCGAGCTCTCTAAAGCCGAGATTAACCTCTACTTGCAGAGGAATT		
Qy	181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePh		
Db	563 GATCAGAAAGCCACGTGACCAAGTCATATCAGATGCACTTTTAGAAGATATTTT		
Qy	201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGl		
Db	623 AATGACCATATGATGTGATGGCTTCATTTCTCCCAAGGAATACAATGATACCA		
Qy	221 GluLeu 222		
Db	683 GAACCTA 688		
RESULT 10			
ADD39771			
ID	ADD39771 standard; cDNA; 907 BP.		
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AC	ADD39771;		
XX			
XX	15-JAN-2004 (first entry)		
XX	Human cDNA encoding secreted/transmembrane protein PRO1304.		
DE			
XX	Human; ss; gene; secreted protein; transmembrane protein; PRO;		
KW	immune response; cardiac insufficiency disorder; calcium flux;		
KW	umbilical vein endothelial cell; bone disorder; cartilage diso;		
KW	arthritis; wound healing; diabetes; skeletal muscle cells; obe		
KW	Berger disease; nephropathy; Schonlein-Henoch purpura; coelac		
KW	dermatitis; herpeticformis; Crohn's disease; thalassemia.		
XX			
OS	Homo sapiens.		

2-Al.

2001US-00013913.
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99WO-US028551.
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2000WO-US000376.
2000WO-US003565.
2000WO-US004342.
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2000WO-US005841.
2000WO-US006884.
2000WO-US013705.
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2000WO-US030952.
2000WO-US030873.
2000WO-US032678.
2001WO-US006520.
2001WO-US006666.
2001WO-US017800.
2001WO-US019692.
2001WO-US021066.
2001WO-US021735.
2001US-00946374.

ENTECH INC.

Botstein D, Desnoyers L, Baton DL, Ferrara N, Fong S, Gird A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Ni NF, Roy MA, Smith V, Stewart TA, Tamas D, Watanabe CK, Wood WI;

55122/71.
39772.

d and transmembrane PRO polypeptides useful for treating dney disorders, Crohn's disease, diabetes mellitus, hyper- or nemia, sports injuries and arthritis.

Q ID NO 179; 557pp; English.

on relates to an isolated PRO polypeptide (secreted or ne protein) having at least 80% amino acid sequence identity acid sequence chosen from 123 fully defined sequences as e specification (including their extracellular domains either their associated signal peptides. Also include are the (NA) sequences encoding PRO, a vector comprising the PRO NA, a comprising the vector, producing PRO, a chimaeric molecule PRO fused to a heterologous amino acid sequence, and an anti-y. PRO is useful as molecular weight markers for protein esis and also for chromosome identification. PRO is also tissue typing. PRO and PRO NA are useful as hybridisation a CDNA library to isolate the full-length PRO CDNA. PRO NA is generating transgenic animals or knock-out animals which are development and screening useful reagents. PRO NA is also ene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are treating cancerous tumours. PRO1250, PRO1418 and PRO1410 s are useful for suppressing immune response. PRO1246 is useful for treating cardiac insufficiency disorders. ypeptide is also useful for treating tumours. PRO1246 and ypeptide are useful for stimulating calcium flux in human

CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474 CC polypeptides are useful for treating bone and/or cartilage disc CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO14 CC polypeptides are useful for treating diabetes in skeletal muscle CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are usef CC treating Berger disease or other nephropathies associated with CC Henoch purpura, coeliac disease, dermatitis, herpetiformis or (CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, CC PRO1410 and PRO1575 are useful in treating thalassaemias. The i CC sequence encodes a PRO protein of the invention.

XX
SQ Sequence 907 BP; 322 A; 160 C; 179 G; 246 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.87e-129	Length:	907
Score:	1189.00	Matches:	222
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-015-480A-180 (1-222) x ADD39771 (1-907)

QY	1	MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTyr
DB	23	ATGCCAAAACCATTCATTCTTATTCAGATTCAATGTTTCTTTTATCTGTG
QY	21	PheThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleGlu
DB	83	TTTACTGCTCAGACACAAAAGAGAGAGAGACCCGAGAAAGTGAATAATAGAF
QY	41	HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAla
DB	143	CATCGTCCAGAAAACCTGCTCTTAAGACAAAGCAAGAGGAGACCTACTAAATGGCC
QY	61	AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsi
DB	203	GACGGCTACCTGGCTAAAGCGGCTCGAAATTTCTACTGACCGCGACACAAA
QY	81	HisProLysThrPheValLeuGlyValGlyGlnValLysLysGlyLeuAspIle
DB	263	CACCCCAAAATGTTTGTCTTGTGGTGGCAAGTATATAAAGGCGCTAGACAT
QY	101	ThrAspMetCysProGlyGluLysArgLysValLysValLysProProSerPheAla
DB	323	ACAGATATGTGCTCGGAGAAAAGCAAGATGATATACCCCTTCAATTTGCG
QY	121	LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGlu
DB	383	AAGGAGGCTATGCAGAAAGCAAGATCCACCGGATGCTACATTGATTTTGA
QY	141	LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAsi
DB	443	CTTTATGCTGTGACCAAGGACCCAGGAGCATTTGAGACATTTAAACCAATAGA
QY	161	AsnAspArgGlnLeuSerLysAlaGluLysLeuLeuLeuGlnArgGluPhe
DB	503	AATGACAGGCGAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAGAGGAATTT
QY	181	AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePhe
DB	563	GATGAGAGCCACCGTACAGTCAATACAGATGCAGTTTATAGAAGATATTTT
QY	201	AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlu
DB	623	AATGACCATGATGTGTGCTTCAATTTCTCCCAAGGAATACAAATGTATACCA
QY	221	GluLeu 222
DB	683	GAACTA 688

RESULT 11
ADD70217

standard; cDNA; 907 BP.

1 (first entry)

encoding secreted/transmembrane protein PRO1304.

gene; secreted protein; transmembrane protein; PRO; tumour;
pense; cardiac insufficiency disorder; calcium flux;
vein endothelial cell; bone disorder; cartilage disorder;
wound healing; diabetes; skeletal muscle cells; obesity;
base; nephropathy; Schonlein-Henoch purpura; coeliac disease;
; herpiformis; Crohn's disease; thalassaemia.

35.

36-Al.

3.

1; 2001US-00006818.

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GCCAAAACCAAGCATTTCTATTACAGATTCATTGTTTCTTTTATCTGTGGGCCCT 82
eThrAlaGluArgGlnIysLysGluGluSerThrGluGluValIysIleGluValLeu 40
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PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
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PR 26-JUL-1999; 99US-0145698P.
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PR 15-SEP-1999; 99WO-US021194.
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PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.

2001WO-US019692.
2001WO-US021066.
2001WO-US021735.
2001US-00946374.

ENTECH INC.

Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
dard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
ni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
Wood WI;

87000/74.
38339.

ted PRO polypeptide, useful for treating cancerous tumors,
ufficiency disorders, wound healing, diabetes mellitus,
s.

Q ID NO 179; 556pp; English.

on relates to an isolated PRO polypeptide (secreted or
ne protein) having at least 80% amino acid sequence identity

: 2.87e-129 Length: 907
1189.00 Matches: 222
ty: 100.00% Conservative: 0
arity: 100.00% Mismatches: 0
100.00% Indels: 0
9 Gaps: 0

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etRAlaGlnArgGlnLysGlnSerThrGluGluValLysGluValLysValLeu 40
TACTGCTCAGACAAAG 142
sArgProGluAsnSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
TGGTCCAGAAACTGCTTAAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 202
pGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
CGGCTACCTGGCTAAAGACGGCTCGAAATTTCTACTGCGCGGACACAAATGAAGGC 262
sProLysThrPheValLeuGlyValGlnValLysGlyLeuAspIleAlaMet 100
CCCCAAATGGTTGTTGTTGGTGTGGGCAAGTCATAAAGGCGCTAGACATTGCTATG 322
rAspMetCysProGlyGlnLysArgLysValLysProProSerPheAlaTyrGly 120
AGATATGTCCTGGAGAAAGCGAAGTAGTATATACCCCTTCATTGTCATACGGA 382
sGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluLeuGlu 140
GGAAGGCTATGCAAGAGCGAAGATTCACCGGATGCTACATTGATTTTTCAGATTGAA 442
uTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
TTATGCTGTGACCAAGGACCGAGCATTTAGACATTATAACCTTCTACTTGCAGAGGAATTGAAAAA 502
nAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
TGACAGGCAGCTCTTAAGACCGAGATAAACCTTCTACTTGCAGAGGAATTGAAAAA 562
pGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
TGAGAAAGCCACGTGACAAGTCATATCAGGATGCGAGTTTTCAGAGATATTTTAAAGAG 622

QY 201 AsnAspHisaspGlyAspGlyPheIleSerProLysGlyTyrAsnValTyrGly
Db 623 AATGACCATGATGGTGATGGCTTCATTCTCCCAAGGAATACAATGTATACCA
QY 221 GluLeu 222
Db 683 GAACATA 688
RESULT 13
ADD39294
ID ADD39294 standard; cDNA; 907 BP.
XX
AC ADD39294;
XX
DT 15-JAN-2004 (first entry)
DE Human cDNA encoding secreted/transmembrane protein PRO1304.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
immune response; cardiac insufficiency disorder; calcium flux;
umbilical vein endothelial cell; bone disorder; cartilage disor
arthritis; wound healing; diabetes; skeletal muscle cells; obes
Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac
dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX
OS Homo sapiens.
XX
FN US2003096954-A1.
XX
PD 22-MAY-2003.
XX
PF 07-DEC-2001; 2001US-00011671.
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PR 01-SEP-1998; 98US-0098716P.
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 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
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 PR 06-JAN-2000; 2000WO-US000376.
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 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
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 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.

(GETH) GENENTECH INC.

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, F.
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hi
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tamas D, W
 PI Williams FM, Wood W;

XX WPI; 2003-786999/74.
 DR P-PSDB; ADD39295.

XX Novel isolated PRO polypeptide useful for tissue typing, modul
 PT biological activity of cell, as molecular weight markers in pr
 PT electrophoresis, for treating arthritis, tumor.

XX Claim 2; SEQ ID NO 179; 550pp; English.

XX The invention relates to an isolated PRO polypeptide (secreted

Alignment Scores:

Pred. No.:	2.87e-129	Length:	907
Score:	1189.00	Matches:	222
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

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 heThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGluValLeu 40
 TTTACTGCTCAGACACAAAGAGAGAGAGACGACGACGAGAGTGAAGTGAAGTTTG 142
 isArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
 ATCGTCCAGAAACCTGCTTAAGACAGCAAGAGAGGAGACCTACTTAAATGCCCATTA 202
 spGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
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 LAGATATGTCCTGGAGAAAGCGAAAGTATATACCCCTTCAATTTGCATACGGA 382
 ysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
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 suTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
 TTTATGCTGTACCAAGACCAAGCAGCATTTGACACATTTAAACAATAGACATGGAC 502
 snAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
 VTGACAGCAGCTCTTAAAGCCGAGATAACCTCTACTTGCMAAGGGAATTTGAAAAA 562
 pGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
 VTGAGAACCCAGTGCAGCAAGTCATATCAGGATGCGAGTTTAAAGATATTTTAAAGAG 622
 snAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAsp 220
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uLeu 222
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 ACTA 688

andard; cDNA; 907 BP.

(first entry)

encoding secreted/transmembrane protein PRO1304.

gene; secreted protein; transmembrane protein; PRO; tumour;
 onase; cardiac insufficiency disorder; calcium flux;
 ein endothelial cell; bone disorder; cartilage disorder;
 wound healing; diabetes; skeletal muscle cells; obesity;
 ase; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 herpetiformis; Crohn's disease; thalassaemia.

S.

1-Al.

XX
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 06-DEC-2001; 2001US-00007194.
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PR	04-SEP-2001;	2001US-00946374.	
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PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hi		
PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, W		
PI	Williams PM, Wood WI;		
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DR	WPI; 2003-765477/72.		
XX	P-PSDB; ADD38818.		
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PT	New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018,		
PT	PRO1244, PRO1246, useful for treating cancerous tumors, cardia		
PT	insufficiency disorders, wound healing, Crchn's disease, celia		
XX			
PS	Claim 2; SEQ ID NO 179; 555pp; English.		
XX			
CC	The invention relates to an isolated PRO polypeptide (secreted		
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(first entry)

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gene; secreted protein; transmembrane protein; PRO; tumour;
onse; cardiac insufficiency disorder; calcium flux;
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wound healing; diabetes; skeletal muscle cells; obesity;
ase; nephropathy; Schonlein-Henoch purpura; coeliac disease;
herpetiformis; Cronn's disease; thalassaemia.

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7-A1.

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GenCore version 5.1.6
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April 9, 2004, 10:47:52 ; Search time 2260 Seconds
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US-10-015-480a-180

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Maximum Match 100%

Listing first 45 summaries

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ter than or equal to the score of the result being printed,
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; APPLICANT: Desnoyers, Luc
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; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurey, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.

Williams, P. Mickey
Wood, William I.
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 TION NUMBER: 60/103633
 DATE: 1998-10-08
 TION NUMBER: 60/103678
 DATE: 1998-10-08
 TION NUMBER: 60/103679
 DATE: 1998-10-08
 TION NUMBER: 60/103711
 DATE: 1998-10-08
 TION NUMBER: 60/104257
 DATE: 1998-10-14
 TION NUMBER: 60/104987
 DATE: 1998-10-20
 TION NUMBER: 60/105000
 DATE: 1998-10-20
 TION NUMBER: 60/105002
 DATE: 1998-10-20
 TION NUMBER: 60/105104
 DATE: 1998-10-21
 TION NUMBER: 60/105169
 DATE: 1998-10-22
 TION NUMBER: 60/105266
 DATE: 1998-10-22
 TION NUMBER: 60/105693
 DATE: 1998-10-26
 TION NUMBER: 60/105694
 DATE: 1998-10-26
 TION NUMBER: 60/105807

Length: 907
 Matches: 222
 ty: 100.00%
 arity: 100.00%
 Mismatches: 0
 Indels: 0
 Gaps: 0

80 (1-222) x US-09-946-374-179 (1-907)

tProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTyrGlyLeu 20
 GCCAAACCATGCTTCTTATTCAGATTCATTGTTTCTTTTATCTGGGCGCTT 82
 eThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleGluValLeu 40
 TACTGCTCAGACACAAAGAAAGAGAGAGAGACCCGAGAGAGTCAAAATAGAGTTTG 142
 sArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
 TGTCTCAGAAACTGCTCTTAAGACAAAGAGAGAGGAGACCTACTAAATGCCATTAT 202
 pGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
 CGGCTACCTGGCTAAAGCGGCTGAAATTTCTACTGCACCGGACACAAATGAGGC 262
 sProLysThrPheValLeuGlyValGlyGlnValLysGlyLeuAspIleAlaMet 100
 CCCCAGATGGTTTGTCTTGTGGTGGCAAGTCAATAAAGGCGCTAGACATTGCTATG 322
 rAspMetCysProGlyGluLysArgLysValLysIleProProSerPheAlaTyrGly 120
 AGATATGTCCTTGGAGAAAGCGAAAGTAGTTATACCCCTTCTATTGTCATCGGA 382
 sGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
 GGAAGGCTATGAGAGAGGCAAGATCCACCGATGCTACATTGATTTTGAATTGAA 442
 uTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160

Db 443 CTTTATGCTGTGACCAAGGACCGAGCATTGAGACATTTAAACAATAGA
 QY 161 AsnAspArgGlnLeuSerIysAlaGluIleAsnLeuTyrLeuGlnArgGluPh
 Db 503 AATGACAGGCGCTCTCTAAAGCCGAGATAAACCTCTACTTCAAAAGGGAAT
 QY 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePh
 Db 563 GATGAGAAGCCACGTCAGCAAGTCATATCAGGATGCGATTTTAGAAGATATTT
 QY 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlu
 Db 623 AATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACATGTATACCA
 QY 221 GluLeu 222
 Db 683 GAACCTA 688

RESULT 2

US-10-006-856A-179
 ; Sequence 179, Application US/10006856A
 ; Publication No. US20030044841A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and I
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830PIC14
 ; CURRENT APPLICATION NUMBER: US/10/006.856A
 ; CURRENT FILING DATE: 2002-05-10
 ; NUMBER OF SEQ ID NOS: 477
 ; Prior Application removed - See File Wrapper or Palm
 ; SEQ ID NO 179
 ; LENGTH: 907
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-006-856A-179

Alignment Scores:
 Pred. No.: 9,97e-148 Length: 907
 Score: 1189.00 Matches: 222
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-10-015-480A-180 (1-222) x US-10-006-856A-179 (1-907)
 QY 1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTyr
 Db 23 ATGCCAAACCATGCTTCTTATTCAGATTCATTGTTTCTTTTATCTGTGG
 QY 21 PheThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleGlu
 Db 83 TTTTACTCTCAGACACAAAGAAAGAGAGAGCACCAGCAAGTGAATAATAGAA
 QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAla
 Db 143 CATCGTCCAGAAACCTGCTCTTAAGACAAAGCAAGAGGAGACCTACTATAATGCC
 QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsn

DB:	14	Gaps:	0
US-10-015-480A-180 (1-222) x US-10-006-818A-179 (1-907)			
QY	1	MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTr	
Db	23	ATGCCAAAACCCANGCATTTCTTTATTCCAGANTCAATGTTTCTTTTATCTGTC	
QY	21	PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleG	
Db	83	TTTACTGCTCAGAGACAAAGAAAGAGGAGAGCACCGAAGAAGTGAATAAG	
QY	41	HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAl	
Db	143	CATCGTCCAGAAACTGCTCTAAGACAAGCAAGGAGGAGACCTTACTAAATGC	
QY	61	AspGlyTyrIleuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAs	
Db	203	GACGGCTACTCGCTTAAGACGGCTCGAAATTTCTACTGCGCCGGACACAAAF	
QY	81	HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIl	
Db	263	CACCCCAATGGTTTGTCTTGTGTGTGGCAAGTCATAAAGAGCCCTAGACAT	
QY	101	ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAl	
Db	323	ACAGATATGTGCCCTGGAGAAAAGCGAAAAAGTAGTTATACCCCTTCATTTCG	
QY	121	LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGl	
Db	383	AAGGAGGCTTATCGAAGAGGCAAGATTCCACCGGATGCTCATTTGATTTTTF	
QY	141	LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs	

Qy	161	AsnAspArgGlnLeuSerIysAlaGluIleAsnLeuTyrLeuGlnArgGluPpT
Db	503	AATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGTCAAAGGGAAAT
Qy	181	AspGluIysProArgaspLysSerTyrGlnAspAlaValLeuGluAspIlePpT
Db	563	GATGAGAAGCCAGTGCACAGTCAATATCAGGATGCAGTCTTTAGAAAGATATTTT
Qy	201	AsnAspHisaspGlyaspGlyPheIleSerProLysGluTyrAsnValTyrGl
Db	623	AATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGATACAAATGATATACCF
Qy	221	GluLeu 222
Db	683	GAACTA 688

RESULT 4
US-10-015-393A-179
US-10-015-393A-179 ; Sequence 179, Application US/10015393A
; Publication No. US20030069179A1

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan J.
APPLICANT: Eaton, Dan J.

APPLICANT: Goddard, Audrey
AFFILIANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
AFFILIANT: Godowski, Paul J.

/ **INVENTOR:** James M. Paoli, Jr.
 /
 / **APPLICANT:** Gurney, Austin L.
 / **APPLICANT:** Hillan, Kenneth J.
 / **APPLICANT:** Paol, James
 / **APPLICANT:** Paoli, Nicholas F.
 / **TITLE OF INVENTION:** Secreted and Transmembrane Polypeptides and
 / Acids Encoding the Same

APPLICANT: FAOHL, NICOLAS F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same

TE: P2830PIC46

CATION NUMBER: US/10/015,393A

IG DATE: 2002-06-10

tion removed - See File Wrapper or Palm

ID NOS: 477

mo sapiens

79

9.97e-148 Length: 907
1189.00 Matches: 222
100.00% Conservativity: 0
100.00% Mismatches: 0
100.00% Indels: 0
14 Gaps: 0

80 (1-222) x US-10-015-393A-179 (1-907)

tProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTrpGlyLeu 20
GCCAATAACCATGATCTTCTTATTCAGATTCATTGTTTCTTTTATCTGCGGCGCTT 82
eThrAlaGlnArgGlnLysGluGluSerThrGluValLysIleGluValLeu 40
TACTGTCTCAGACACAAAGAGAGGAGACCGAAGAGAGTGAATAATGAAATTTTG 142
sArgProGluAspCysSerLysThrSerLysGlyAspLeuAsnAlaHisTyr 60
TCTGTCAGAAATCTGCTTAAGACAGCAAGAGAGGAGACCTACTAAATGCCATTAT 202
pGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
CGGCTACCTGGCTAAAGAGCGCTCGAAATCTACTGCGCGGACACAAATGAGGC 262
sProLysThrPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMet 100
ACCCCAATGATGTTTCTTCTGCTGTTGGCAAGTCATAAAGGCGCTAGACATTGCTATG 322
rAspMetCysProGlyGlnLysArgLysValValIleProProSerPheAlaTyrGly 120
TAGATATGTCCTCGGAGAAAGCGAAAGTAGTTATACCCCTTCAATTTTCATACGGA 382
sGluGlyTyrAlaGluLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
GGAAGCTATGCGAAGGCAAGATTCACCGGATGCTACATTGATTTTTCAGATTGAA 442
uTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
TTATGCTGTGACCAAGGACCGGAGCATTTGAGACATTTAAACAAATGACATGGAC 502
nAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
TGACAGGCGCTCTCTAAGCCGAGAAACCTCTACTTCAAGAGGAAATTTGAAAAA 562
pGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
TGAGAGCCACGTGACAAAGTCATATCAGGATGCGATTTTGAAGATATTTTAAAGAG 622
nAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAsp 220
ATGACCATGATGATGCTTCTTCTCCAGGAATCAATGTATATACCAACCATGAT 682

uLeu 222

ACTA 688

79

Application US/10015869A

US20030073130A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PIC45
CURRENT APPLICATION NUMBER: US/10/015,869A
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 179
LENGTH: 907
TYPE: DNA
ORGANISM: Homo sapiens
US-10-015-869A-179

Alignment Scores:

Pred. No.: 9.97e-148 Length: 907
Score: 1189.00 Matches: 222
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-10-015-480A-180 (1-222) x US-10-015-869A-179 (1-907)

Qy 1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTr
Db 23 ATGCCAATAACCATGATCTTCTTATTCAGATTCATTGTTTCTTTTATCTGTG
Qy 21 PheThrAlaGlnArgGlnLysGluGluSerThrGluGluValLysIleGln
Db 83 TTTACTGTCTCAGACACAAAGAGAGGAGACCGAAGAGTCAAAATAGA
Qy 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuAsnAl
Db 143 CATGCTCCAGAAATCTGCTCTAAGACAAAGAGGAGGAGACCTACTAAATGCG
Qy 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAs
Db 203 GACGCTACCTGGCTAAAGACGGCTCGAAATTTCTACTGACGCGGACACAAA
Qy 81 HisProLysThrPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIle
Db 263 CACCCCAATGTTTCTTCTGCGCAAGTCATAAAGAGGCGCTAGACATT
Qy 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAl
Db 323 ACAGATATGTCCTCGGAGAAAGCGAAAGTAGTTATACCCCTTCAATTTGCG
Qy 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGln
Db 383 AAGGAGGCTATGCGAAGGCAAGATCCACCGGATGCTACATTGATTTTGA
Qy 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs
Db 443 CTTTATGCTGTGACCAAGAGGACCGAGCATTCAGACATTATAACAAATAGA
Qy 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPhe
Db 503 AATGACAGGCGAGCTCTCTAAAGCGGAGATAAACCTCTACTTGCAGAGGGAATTT

spGluysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLys 200
 ATGAGAAGCCAGTCGACAAAGTCATATCAGATGCGAGTTTITAGAGATATTTTAAAGAAG 622
 sAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAsp 220
 ATGACCATGATGGTGATGCTTCATTTCTCCCAAGGAATACAAATGTATACCAACGAT 682
 lueu 222
 AACTA 688

179
 Application US/10012121A
 C. US20030073810A1
 MARION:
 aker, Kevin P.
 Botstein, David
 Desnoyers, Luc
 Eaton, Dan I.
 Ferrara, Napoleone
 Fong, Sherman
 Gao, Wei-Qiang
 Goddard, Audrey
 Grimaldi, Paul J.
 Gurney, Austin L.
 Hillan, Kenneth J.
 Pan, James
 Paoni, Nicholas F.
 ENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ENTION: Acids Encoding the Same
 CE: P2830P1C20
 ICATION NUMBER: US/10/012.121A
 NG DATE: 2001-12-07
 ation removed - See File Wrapper or Palm
 Q ID NOS: 477

omo sapiens
 179

S: 9.97e-148 Length: 907
 1189.00 Matches: 222
 ity: 100.00% Conservative: 0
 larity: 100.00% Mismatches: 0
 100.00% Indels: 0
 14 Gaps: 0

180 (1-222) x US-10-012-121A-179 (1-907)

etProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTrpGlyLeu 20
 TGCCAAAACCAACGATCTTCTTATTCAGATTCATTTGTTTCTTTATCTGTGGGCGCTT 82
 heThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleGluValLeu 40
 TTACTGCTCAGACACAAAAGAAAGAGAGAGACCCGAGAAAGTGAATAAGAGTTTGT 142
 tisArgProGluAnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
 ATCGTCAGAAAACCTGCTCTTAACACAGCAGGAGGAGACCTACTAAATGCCCATAT 202
 aspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
 AACGGCTACCTGGTAAAGACGGCTCGAAATCTACTGCGAGCCGAGACACAAATGAAGGC 262
 tisProLysTrpPheValLeuGlyValGlyGlnValLysGlyLeuAspIleAlaMet 100

Db 263 CACCCCAATGGTTTCTTCTGTGTGGCAAGTCATATAAAGGCCTAGACAI
 QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAl
 Db 323 ACAGATATGTGGCCTCGAGAAAAGCGAAAGTAGITATACCCCTTCATTTGC
 QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGly
 Db 383 AAGGAAGGCTATGCAGAGGCAAGATTCCACCGGATGCTACATTGATTTTGA
 QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs
 Db 443 CTTTATGCTGTGACCAAGGACCCAGGACGATTTTAAACAAATAGA
 QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPh
 Db 503 ATGCAGAGCAGCTCTCTTAAGCCGAGATAAACCTCTACTTGCAGAGGATTT
 QY 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePh
 Db 563 GATGAGAAGCCAGTCGACAAAGTCATATCAGGATGCGAGTTTITAGAGATATTT
 QY 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGly
 Db 623 AATGACCATGATGGTGATGCTTCATTTCTCCCAAGGAATACAAATGTATACCA
 QY 221 GluLeu 222
 Db 683 GAACTA 688

RESULT 7
 US-10-006-116A-179
 : Sequence 179, Application US/10006116A
 : Publication No. US20030082626A1
 : GENERAL INFORMATION:
 : APPLICANT: Baker, Kevin P.
 : APPLICANT: Botstein, David
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Eaton, Dan I.
 : APPLICANT: Ferrara, Napoleone
 : APPLICANT: Fong, Sherman
 : APPLICANT: Gao, Wei-Qiang
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, Christopher J.
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Hillan, Kenneth J.
 : APPLICANT: Pan, James
 : APPLICANT: Paoni, Nicholas F.
 : TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
 : TITLE OF INVENTION: Acids Encoding the Same
 : FILE REFERENCE: P2830P1C15
 : CURRENT APPLICATION NUMBER: US/10/006,116A
 : CURRENT FILING DATE: 2001-12-16
 : PRIOR APPLICATION NUMBER: 60/098716
 : PRIOR FILING DATE: 1998-09-01
 : PRIOR APPLICATION NUMBER: 60/098723
 : PRIOR FILING DATE: 1998-09-01
 : PRIOR APPLICATION NUMBER: 60/098749
 : PRIOR FILING DATE: 1998-09-01
 : PRIOR APPLICATION NUMBER: 60/098750
 : PRIOR FILING DATE: 1998-09-01
 : PRIOR APPLICATION NUMBER: 60/098803
 : PRIOR FILING DATE: 1998-09-02
 : PRIOR APPLICATION NUMBER: 60/098821
 : PRIOR FILING DATE: 1998-09-02
 : PRIOR APPLICATION NUMBER: 60/098843
 : PRIOR FILING DATE: 1998-09-02
 : PRIOR APPLICATION NUMBER: 60/099536
 : PRIOR FILING DATE: 1998-09-09
 : PRIOR APPLICATION NUMBER: 60/099596
 : PRIOR FILING DATE: 1998-09-09
 : PRIOR APPLICATION NUMBER: 60/099598

DATE: 1998-09-09
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DATE: 1998-09-23

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TION NUMBER: 60/101916
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TION NUMBER: 60/102207
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TION NUMBER: 60/102331
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TION NUMBER: 60/102687
DATE: 1998-10-01
TION NUMBER: 60/102965
DATE: 1998-10-02
TION NUMBER: 60/103258
DATE: 1998-10-06
TION NUMBER: 60/103314
DATE: 1998-10-07
TION NUMBER: 60/103315
DATE: 1998-10-07
TION NUMBER: 60/103328
DATE: 1998-10-07
TION NUMBER: 60/103395
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TION NUMBER: 60/103396
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TION NUMBER: 60/103679
DATE: 1998-10-08
TION NUMBER: 60/103711
DATE: 1998-10-08
TION NUMBER: 60/104257
DATE: 1998-10-14
TION NUMBER: 60/104987
DATE: 1998-10-20
TION NUMBER: 60/105000
DATE: 1998-10-20
TION NUMBER: 60/105002
DATE: 1998-10-20
TION NUMBER: 60/105104
DATE: 1998-10-21
TION NUMBER: 60/105169
DATE: 1998-10-22
TION NUMBER: 60/105266

DATE: 1998-10-22
 ATION NUMBER: 60/105693
 DATE: 1998-10-26
 ATION NUMBER: 60/105694
 DATE: 1998-10-26
 ATION NUMBER: 60/105807
 DATE: 1998-10-27
 ATION NUMBER: 60/105881
 DATE: 1998-10-27
 ATION NUMBER: 60/105892
 DATE: 1998-10-27
 ATION NUMBER: 60/106023
 DATE: 1998-10-28

3: 9.97e-148 Length: 907
 1189.00 Matches: 222
 Conservativity: 0
 Identity: 100.00% Mismatches: 0
 Indels: 0
 Gaps: 14

180 (1-222) x US-10-006-116A-179 (1-907)

atProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTrpGlyLeu 20
 TSCCAAAAACCATGCTATTTCTTATTCAGATTCATTGTTTCTTTTATCTGTGGGCCCTT 82
 aeThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysLysLeuValLeu 40
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isArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
 ATGCTCCAGAAAACCTGCTCTAGACACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 202
 spGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
 ACGGCTACCTGGCTAAAGACGCGCTCGAATTTCTACTGCGAGCGGACACAAATGAAGGC 262

isProLysTrpPheValLeuGlyValGlyGlnValLysLysGlyLeuAspIleAlaMet 100
 ACCCCAAAATGGTTGTTCTTGTGTTGGCAAGTCTAAAGAGCGCTAGACATTGCTATG 322
 hrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAlaTyrGly 120
 CAGATATGTGCTGGAGAAAAGCGAAGTAGTATATACCCCTTCATTGTGCTACGGA 382

ysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
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 TTTATGCTGTGACCAAGAGACCCAGGAGCATTTAGACATTTTAAACAAATAGACATGGAC 502

snAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
 ATGACAGCGCGCTCTCTAAAGCCGAGATAAACCTTACTTTGCAAGGGAGATTGAAAGA 562
 spGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
 ATGAGAAGCCACGTGACAAAGTCATATCAGGATGCAGTTTGTAGAGATATTTTAAAGAG 622

snAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAsp 220
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US-10-006-117A-179
 ; Sequence 179, Application US/10006117A
 ; Publication No. US20030082827A1
 ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
 ; FILE REFERENCE: P2830P1C13
 ; CURRENT APPLICATION NUMBER: US/10/006,117A
 ; Prior Filing DATE: 2002-03-19
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 477
 ; SEQ ID NO 179
 ; LENGTH: 907
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-006-117A-179

Alignment Scores:
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 Score: 1189.00 Matches: 222
 Percent Similarity: 100.00% Conservativity: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-10-015-480A-180 (1-222) x US-10-006-117A-179 (1-907)

QY 1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTr
 Db 23 ATGCCAAAACCATGCTATTTCTTATTCAGATTCATTGTTTCTTTTATCTGTG
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 QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAl
 Db 143 CATGCTCCAGAAAACCTGCTTAAGACACAGAGAGAGAGAGAGAGAGAGAGAGAG
 QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAs
 Db 203 GACGGCTACCTGGCTAAAGACGCGCTCGAATTTCTACTGCGAGCGGACACAAAA
 QY 81 HisProLysTrpPheValLeuGlyValGlyGlnValLysLysGlyLeuAspIle
 Db 263 CACCCCAAAATGGTTTGTCTTGTGTTGGCAAGTCATAAAAGGCGCTAGACAT
 QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAl
 Db 323 ACAGATATGTGCTGGAGAAAAGCGAAGTAGTATATACCCCTTCATTGTC
 QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGln
 Db 383 AAGGAAGGCTATGCAGAGGCAAGATTCACCGGATGCTACATTGATTTTGA
 QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs
 Db 443 CTTTATGCTGTGACCAAGAGGACCGAGGATTTGAGACATTTTAAACAAATAGA

uLeu 222
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ACTA 688

TION NUMBER: 60/098716
DATE: 1998-09-01
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 DATE: 1998-10-26
 ATION NUMBER: 60/105694
 DATE: 1998-10-26
 ATION NUMBER: 60/105807
 DATE: 1998-10-27
 ATION NUMBER: 60/105881
 DATE: 1998-10-27
 ATION NUMBER: 60/105882
 DATE: 1998-10-27
 ATION NUMBER: 60/106023
 DATE: 1998-10-28

Alignment Scores: 9.97e-148 Length: 907
 Pred. No.: 1189.00 Matches: 222
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 100.00% Gaps: 0
 DB: 14

US-10-015-480a-180 (1-222) x US-10-017-527A-179 (1-907)

Qy 1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTyr
 Db 23 ATGCCAAACCATGCAATTCATTATTCAGATTCAATGTTTCTTTATCTGTC
 Qy 21 PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleG
 Db 83 TTTTACTGCTCAGACACAAAAGAAAGAGAGAGACCCGCAAGAGTGAATAATAG
 Qy 41 HisArgProGluAsnCysserLysThrSerLysLysGlyAspLeuLeuAsnAl
 Db 143 CATCGTCCAGAAAACCTGCTTAAGCAAGCAAGAGAGAGACCTACTAAATGC
 Qy 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAs
 Db 203 GACGGCTACTGGCTAAAGACGCTCGAAATTCCTACTGCAGCCGGACACAAA
 Qy 81 HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIl
 Db 263 CACCCCAATGTTTCTTCTTGGTGTGGGCAAGTCTATAAAGCCCTAGACAI
 Qy 101 ThrAspMetCysProGlyGluLysArgLysValValIleProSerPheAl
 Db 323 ACAGATATGTCCTCGAGAAAAGCCGAAAGTAGTATTATACCCCTTCATTTC
 Qy 121 LysGluGlyTyrAlaGluGlyLysIleProAspAlaThrLeuIlePheG
 Db 383 AAGGAAGGCTATGCAGAAAGCAAGATTCCACCGGATGTACATTGATTTTGA
 Qy 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs
 Db 443 CTTTATGCTGTGACCAAGACCAAGAGCAGGAGCATTGAGACATTTAAACAAATAG
 Qy 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluP
 Db 503 AATGACAGCAGGCTCTTAAGCCGAGATAAACCTCTACTTGCAGAGGAAAT
 Qy 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePh
 Db 563 GATGAGAAGCCACGTGACAAAGTCAATATCAGGATGCAGATTTTAGAGATATTT
 Qy 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrG
 Db 623 AATGACCATGAGGTGATGCTTCATTCTCCCAAGAAATACAAATGTATACCA
 Qy 221 GluLeu 222
 Db 683 GAACTA 688

RESULT 10
 US-10-013-913A-179
 ; Sequence 179, Application US/10013913A
 ; Publication No. US20030083462A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.

Grimaldi, Christopher J.
 Gurney, Austin L.
 Hillan, Kenneth J.
 Pan, James
 Paoni, Nicholas F.
 INTION: Secreted and Transmembrane Polypeptides and Nucleic
 INTION: Acids Encoding the Same
 E: P2830PIC40
 :CATION NUMBER: US/10/013,913A
 IG DATE: 2002-07-15
 ition removed - See File Wrapper or Palm
 ID NOS: 477

omo sapiens
 .79

9.97e-148 Length: 907
 1189.00 Matches: 222
 100.00% Conservativity: 0
 100.00% Mismatches: 0
 100.00% Indels: 0
 14 Gaps: 0

80 (1-222) x US-10-013-913A-179 (1-907)

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 |||||
 TCGTCCAGAAACCTGCTTAAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 202
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Db 683 GAACTA 688

RESULT 11

US-10-007-194A-179
 ; Sequence 179, Application US/10007194A
 ; Publication No. US20030092061A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830PIC6
 ; CURRENT APPLICATION NUMBER: US/10/007,194A
 ; CURRENT FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: 60/098716
 ; PRIOR FILING DATE: 1998-09-01
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; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Alignment Scores:

Pred. No.:	9.97e-148	Length:	907
Score:	1189.00	Matches:	222
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-015-480a-180 (1-222) x US-10-007-194A-179 (1-907)

Qy	1	MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTr
Db	23	ATGCCAAACCAACGATTCATTATTCAGATTCATTTCTTTTATCTGIG

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.TTATGCTGTGACCAAGAGGACCGAGCATTGAGACATTTAAACAAATAGACATGGAC 502
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uLeu 222
ACTA 688

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79 Application US/10013430A

US20030092883A1

ATION:

ker, Kevin P.

otstein, David

esnoyers, Luc

aton, Dan I.

errara, Napoleone

tong, Sherman

ao, Wei-Qiang

oddard, Audrey

odowski, Paul J.

rimaldi, Christopher J.

urney, Austin L.

illan, Kenneth J.

an, James

moni, Nicholas F.

NTION: Secreted and Transmembrane Polypeptides and Nucleic

NTION: Acids Encoding the Same

E: P2830PIC31

CATION NUMBER: US/10/013,430A

IG DATE: 2002-06-25

tion removed - See File Wrapper or Palm

ID NOS: 477

TYPE: DNA
ORGANISM: Homo sapiens
US-10-013-430A-179

Alignment Scores:

Pred. No.: 9,97e-148 Length: 907
Score: 1189.00 Matches: 222
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-015-480A-180 (1-222) x US-10-013-430A-179 (1-907)

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Db 23 ATGCCAAATGCTTCTTATTCAGATTCAATGTTCTTTTATCTGTTG
QY 21 PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGlu
Db 83 TTTACTGCTCAGACACAAAGAAAGAGGAGAGCACCAGAGAAAGTGAATAAGA
QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAla
Db 143 CATGCTCCAGAAAACCTGCTCTAAGACAAAGCAAGCAAGAGGAGACCTACTAAATGC
QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsn
Db 203 GACGCTACCTGGCTTAAAGACGGCTCGAAATTTCTACTGACCGCGGACACAAA
QY 81 HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIle
Db 263 CACCCCAATGCTTGTGTTCTTGGTGTGGCAAGTCATATAAAGGCGCTAGACAT
QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheAla
Db 323 ACAGATATGCTGCTCGAGAAAAGGCAAGATTCACCGGATGCTACATGATTTTGA
QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGlu
Db 383 AAGGAAGCCTATGACAGAGGCAAGATTCACCGGATGCTACATGATTTTGA
QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAsn
Db 443 CTTTATGCTGTGACCAAGAGGACCGAGGATTCAGACATTTAAACAAATAGA
QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPhe
Db 503 AATGACAGCGAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAGAGGGAATT
QY 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePhe
Db 563 GATGAGAAAGCCACGCTGACCAAGTCATATCAGGATGCGATTTTAGAAGATATTTT
QY 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlu
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QY 221 GluLeu 222
Db 683 GAACTA 688

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RESULT 13

US-10-011-671A-179
Sequence 179, Application US/10011671A
Publication No. US20030096954A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman

Gao, Wei-Qiang
Soddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
ENTION: Secreted and Transmembrane Polypeptides and Nucleic
ENTION: Acids Encoding the Same
CE: F2830F1C27
ICATION NUMBER: US/10/011.671A
NG DATE: 2002-06-10
ATION NUMBER: 60/098716
DATE: 1998-09-01
ATION NUMBER: 60/098723
DATE: 1998-09-01
ATION NUMBER: 60/098749
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 ATION NUMBER: 60/105807
 DATE: 1998-10-27
 ATION NUMBER: 60/105881
 DATE: 1998-10-27
 ATION NUMBER: 60/105882
 DATE: 1998-10-27
 ATION NUMBER: 60/106023
 DATE: 1998-10-28

9.97e-148 Length: 907
 1189.00 Matches: 222
 100.00% Conservativity: 0
 100.00% Mismatches: 0
 100.00% Indels: 0
 14 Gaps:

80 (1-222) x US-10-011-671A-179 (1-907)

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 SCCTAAACCATGCTTCTTATTCAGATTCATGTTTCTTTTATCTGGGGCTT 82
 eThrAlaGlnArgGlnLysGluSerThrGluGluValLysIleGluValLeu 40
 TACTGCTCAGACAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 142
 sArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
 TCGTCAGAAAACCTGCTCTAAGCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 202
 pGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
 CGGCTACCTGGCTAAGACGGCTCGAATCTTACTGACCCGAGACAAATGAAGGC 262
 sProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMet 100

Db 263 CACCCCAATGTTTGTCTTGGTGGCAAGTCATAAAAGGCGCTAGACAT
 QY 101 ThrAspMetCysProGlyGlyLysValValIleProProSerPheAl
 Db 323 ACAGATATGTGCGCTGGAGAAAAGCAAGTAGTTATACCCCTTCATTTC
 QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheG
 Db 383 AAGGAAGGCTATGCAGAGGCAAGATTCACCGGATGCTACATTCATTTCGA
 QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs
 Db 443 CTTTATGCTGTGACCAAGGACCAGGAGCATTCAGACATTTAAACAAATAGA
 QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPh
 Db 503 AATGACAGGCGAGCTCTCTAAAGCCGAGATAAACCTCTACTTCAAAAGGGAATT
 QY 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePh
 Db 563 GATGAGAAGCCACCGTCAAGTCATATCAGGATGCGAGTTTATAGAAAGATATTT
 QY 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlu
 Db 623 AATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACATGTATACCA
 QY 221 GluLeu 222
 Db 683 GAACTA 688

RESULT 14

US-10-012-755A-179
 ; Sequence 179, Application US/10012755A
 ; Publication No. US20030096955A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830PIC28
 ; CURRENT APPLICATION NUMBER: US/10/012.755A
 ; CURRENT FILING DATE: 2002-06-10
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 477
 ; SEQ ID NO 179
 ; LENGTH: 907
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-012-755A-179

Alignment Scores:
 Pred. No.: 9.97e-148 Length: 907
 Score: 1189.00 Matches: 222
 Percent Similarity: 100.00% Conservativity: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0
 US-10-015-480A-180 (1-222) x US-10-012-755A-179 (1-907)


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PheThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleGluValLeu 40
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TTTACTGCTCAGAGCAAAAGAAAGAGAGAGACCCGAAAGAGTGAATAATGAAAGTTTGT 142
|||||
HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
|||||
TATCGTCAGAAAACCTGCTTAAGACAGCAAGAGGAGGACCTACTTAATAGCCCATAT 202
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AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
|||||
TACGGCTACCTGGCTAAAGACGGCTCGAAATTTCTACTCAGCGGACACAAAATGAAAGGC 262
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TACCCCAATAGTTTGTCTTGTGTTGGGCAAGTCATAAAAGGCGCTAGACATTGCTATG 322
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ThrAspMetCysProGlyGluLysArgLysValValLysProProSerPheAlaTyrGly 120
|||||
ACAGATATGTCCTGGAGAAAGCGAAAGTAGTTATACCCCTTCTATTTGCTATACGGA 382
|||||
LysGluGlyTyrAlaGluGlyLysIleProAspAlaThrLeuIlePheGluIleGlu 140
|||||
TAGGAAGCTATGACAGAAAGCAAGATTCACCGGATGCTACATTCATTTTGAGATTGAA 442
|||||
LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
|||||
TTTATGCTGTGACCAAGGACCGGAGCATTTAGACATTTAAACAAATAGACATGGAC 502
|||||
AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
|||||
LATGACAGCGAGCTCTCTAAAGCGGAGATAAACCTCTACTTGCAGAGGGAATTTGAAAA 562
|||||
AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
|||||
TATGAGAGCCACCGTGACAACTCATATCAGGATGCAGTTTAAAGATATTTTAAAGAG 622
|||||
AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrGlnHisAsp 220
|||||
LATGACCATGATGGTGATGGCTTCTATCTCCCAAGGAATACATGTATACCAACAGAT 682
|||||
GluLeu 222
|||||
HAACTA 688

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179 Application US/10015386A
180 No. US20030099625A1
181 JNATION:
182 Baker, Kevin P.
183 Botstein, David
184 Desnoyers, Luc
185 Eaton, Dan I.
186 Ferrara, Napoleone
187 Fong, Sherman
188 Gao, Wei-Qiang
189 Goddard, Audrey
190 Godowski, Paul J.
191 Grimaldi, Christopher J.
192 Gurney, Austin L.
193 Hillan, Kenneth J.
194 Pan, James
195 Paoni, Nicholas F.
196 JENION: Secreted and Transmembrane Polypeptides and Nucleic
197 JENION: Acids Encoding the Same
198 ICE: P2830PIC55
199 JICATION NUMBER: US/10/015,386A
200 NG DATE: 2001-12-12
201 ation removed - See File Wrapper or Palm

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; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 179
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-386A-179

Alignment Scores:
Pred No.: 9,97e-148 Length: 907
Score: 1189.00 Matches: 222
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-015-480A-180 (1-222) x US-10-015-386A-179 (1-907)

QY 1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTyr
DB 23 ATGCCAAAAACCATGCAATCTCTTAATTCAGATTCAATGTTCTTTTCTTTTCTG
QY 21 PheThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleG
DB 83 TTTACTGCTCAGAGCAAAAGAAAGAGGAGGACCCGAAAGAGTGAATAATG
QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnA
DB 143 CATGCTCCAGAAAACCTGCTTAAGACAGCAAGAGGAGGACCTACTTAATG
QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnA
DB 203 GACGGCTACCTGGCTAAAGACGGCTCGAAATTTCTACTGCGGCGGACACAAA
QY 81 HisProLysTyrPheValLeuGlyValGlyGlnValLysLysGlyLeuAspI
DB 263 CACCCCAATGGTTGTTCTTGGTGGCAAGTCATAAAAGGCGCTAGACA
QY 101 ThrAspMetCysProGlyGluLysArgLysValValLysProProSerPheA
DB 323 ACAGATATGTCCTCGAGAAAGCGAAAGTAGTTATACCCCTTCTCATTTG
QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheG
DB 383 AAGGAAGGCTATGCAAGGCAAGATTCCACCGGATGCTACATTTGATTTTG
QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleA
DB 443 CTTTATGCTGTGACCAAGGACCCAGGAGCATTTGAGACATTTAAACAAATAG
QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluP
DB 503 AATGACAGCGAGCTCTCTAAAGCGGAGATAAACCTCTACTTGCAGAGGAAT
QY 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIleP
DB 563 GATGAGAGGCGGACGTGCAAGTCAATATCAGGATGCGAGTTTATAGAGATATTT
QY 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrG
DB 623 AATGACCATGATGGTGATGGCTTCTATCTCCCAAGGAATACATGTATACCA
QY 221 GluLeu 222
DB 683 GAACTA 688

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Search completed: April 9, 2004, 13:29:29
Job time : 2273 secs

10:32:16 2004

us-10-015-480a-180.rst

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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April 9, 2004, 10:39:09 ; Search time 3101 Seconds
(without alignments)
2137.828 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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hits satisfying chosen parameters: 55026578
length: 0
ength: 2000000000
Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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EST:*
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2: em_esthum.*
3: em_estin.*
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6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
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21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_xod.*
26: em_gss_pbg.*
27: em_gss_vrl.*
28: gb_gss1.*
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29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have
score greater than or equal to the score of the result being
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1121	94.3	800	12	BI827688	BI827688
5	1085	91.3	643	12	EG939266	EG939266
6	1079	90.7	943	14	CD557479	CD557479
7	1010	85.0	734	10	BE874396	BE874396
8	936	78.8	734	14	CB570987	CB570987
9	935	78.6	618	14	CF794142	CF794142
10	929	78.1	602	13	BU551693	BU551693
11	908	76.4	602	13	EX485892	EX485892
12	890	74.9	800	14	CB959508	CB959508
13	865	72.8	604	12	BI964616	BI964616
14	856	72.0	644	12	EG896952	EG896952
15	837	70.4	673	9	AI182368	AI182368
16	832	70.0	546	10	BE756310	BE756310
17	817	68.7	861	13	BU400194	BU400194
18	817	68.7	922	13	BU135960	BU135960
19	813	68.4	884	13	BU253965	BU253965
20	809	68.0	647	13	BU300409	BU300409
21	805	67.7	769	13	BU319076	BU319076
22	803	67.6	748	14	CB573983	CB573983
23	803	67.5	672	12	BM488556	BM488556
24	803	67.5	690	14	CA412939	CA412939
25	800	67.3	867	13	BU320661	BU320661
26	799	67.2	856	13	BU405087	BU405087
27	792	66.6	618	12	EG939267	EG939267
28	790	66.5	553	14	CF112806	CF112806
29	786	66.1	1026	13	BU356231	BU356231
30	783	65.9	498	9	AA457921	AA457921
31	772	64.9	643	14	CF792774	CF792774
32	771	64.8	521	9	AW082138	AW082138
33	766	64.5	699	14	CF794309	CF794309
34	764	64.3	889	13	BU359419	BU359419
35	760	64.0	457	9	AI879695	AI879695
36	760	63.9	811	10	BF210667	BF210667
37	753	63.3	893	13	BU128923	BU128923
38	747	62.8	755	13	BU136444	BU136444
39	745	62.7	517	9	AV745382	AV745382
40	734	61.7	550	13	EX515852	EX515852
41	719	60.5	488	10	BF604773	BF604773
42	719	60.5	506	10	BE850956	BE850956
43	717	60.3	775	13	BU299669	BU299669
44	712	59.9	636	14	CA313338	CA313338
45	709	59.6	646	10	BF179938	BF179938

ALIGNMENTS

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RESULT 1
AF092137
LOCUS AF092137 1231 bp mRNA linear HTC
DEFINITION Homo sapiens FK506-binding protein mRNA, complete cds.
ACCESSION AF092137
VERSION AF092137.1 GI:5138923
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hor
REFERENCE 1 (bases 1 to 1231)
AUTHORS Han,Z., Song,H., Dai,M., Huang,Q., Mao,Y., Zhang,Q., Mac
```

M., Chen, J. and Hu, R.
an FK506-binding protein mRNA, complete cds
(bases 1 to 1231)

ect Submission
mitted (16-SEP-1998) Shanghai Second Medical University, Rui-Jin
pital, Shanghai Institute of Hematology, 197 Rui-Jin Road II,
anghai 200025, P.R. China
Location/Qualifiers

1. .1231
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal pituitary"
85. .753
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/product="FK506-binding protein"
/protein_id="AAD40379.1"
/db_xref="GI:5138924"
/translation="MPKTMHFLFRFIVFFYLMGLFTAQRQKKEESTEEVKIEVLHPE
NCSKTSKGLLNAYDGLAKDSKFYCSRTQNEHPKWFVLGVGVIGKGLDIAMTD
MCPGEKRWIPPSFVKGKGHAGKIPDPATLIFELVAVTKGPRSIFTEKIDMD
NDROLSKAEINLYLQREFEDEXPRDKSYQDAVLEDFKKNDDHGDGDFISPKYENVYQ
HDEL"

S: 3.03e-119 Length: 1231
1184.00 Matches: 221
ity: 100.00% Conservative: 1
arity: 99.55% Mismatches: 0
99.58% Indels: 0
11 Gaps: 0

180 (1-222) x AF092137 (1-1231)

etProlysthrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTyrGlyLeu 20
TGCACAAACCAATGCAATTCATTATTCAGATTCATTGTTCTTTATCTGTGGGCTT 144
heThrAlaGlnArgGlnLysLysGluSerThrGluGluValLysIleGluValLeu 40
TACTCTCAGACACAAAGAAAGAGAGAGACCCGAAAGAGTGAATAGAGTTTG 204
isArgProGluAsnGlySerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
ATCGTCAGAAAACCTGCTTAGACAAAGCAAGAGGAGACCTACTAAATGCCATTAT 264
spGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
ACGGCTACCTGGCTAAGAGCGGCTCGAAATTTCTACTGCAGCCGACACAAATGAAGGC 324
isProlysthrPheValLeuGlyValGlyGlnValLysGlyLeuAspIleAlaMet 100
ACCCCAATAGTTGTTCTTCTGTTGGCAAGTCAATAAAGCCCTAGACATGCTATG 384
hrAspMetCysProGlyGluLysArgLysValValleProProSerPheAlaTyrGly 120
CAGATATGTCCTGAGAAAAGCGAAAGTAGTATTATACCCCTTCTATTGTCATACGGA 444
ysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
AGGAAGCCCATGACAGAAAGCAAGATTCCACCGGATGCTACATTGATTTTGATTTGAA 504
eufTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
TTTATGCTGTGACCAAGAGCCAGGAGCATTTGAGACATTTAAACAAAATAGACATGAC 564
snAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
ATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAGAAAGGAATTTGAAAA 624

QY 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIleP 1
Db 625 GATGAGAAGCCACGTGACAAAGTCATATCAGATGCAGCTTTTAGAAGATATT 1
QY 201 AsnAspHisAspGlyAspGlyPheIleSerProLysGluTyrAsnValTyrG 1
Db 685 AATGACCATGATGTTGATGCTTCATTCTCCCAAGGAATACAAATGTATACC 1
QY 221 GluLeu 222 1
Db 745 GAACTA 750 1

RESULT 2
CF593540

LOCUS
DEFINITION
AGENCOURT 15624003 NIH MGC 147 Homo sapiens cDNA clone
IMAGE:30531031 5', mRNA sequence.

ACCESSION
CF593540
VERSION
CF593540.1 GI:36347183

KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; HC

REFERENCE
1. (bases 1 to 786)
NIH-MGC http://mgs.nci.nih.gov/.

AUTHORS
TITLE
JOURNAL
COMMENT
National Institutes of Health, Mammalian Gene Collectic
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs-i@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

cDNA Library Preparation: Michael J. Brownstein (NHGRI
and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LI
DNA sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution informatior
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM621 row: c column: 08

High quality sequence stop: 623.

FEATURES
source

1. .786
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30531031"
/tissue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 147"
/notes="Organ: placenta; Vector: pBluescriptR;
all-XhoI; Site 2: BamH; Oligo-dT primed using
5'-TTTTTTTTTTTTTTVN-3', size-selected for a
insert size 2.3 kb and normalized to ROT 5. Tl
primary library enriched for full-length clone
constructed using the Cap-trapper method (Car
(NIMH/NHGRI, National Institutes of Health). N
a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.: 2,78e-115 Length: 786
Score: 1146.00 Matches: 221
Percent Similarity: 98.67% Conservatives: 1
Best Local Similarity: 98.22% Mismatches: 0
Query Match: 96.38% Indels: 3
DB: 14 Gaps: 0

US-10-015-480A-180 (1-222) x CF593540 (1-786)

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 |||||
 GCACAAACCATGATCTTATTCAGATTCATTTCTTTTATCTGGGCGCTT 160
 |||||
 leThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGluValLeu 40
 |||||
 TACTGCTCAGACACAAAGAGGAGAGACCCGAAAGAGTGAATAGAGTTTG 220
 |||||
 sArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyr 60
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 TCGTCCAGAAACCTGCTTAAGACAAGCAAGAGGAGACCTACTAATGCCCATAT 280
 |||||
 pGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
 |||||
 CGGCTACTCGCTAAAGACGGCTCGAAATTTCTACTGACGGCGGACACAAATGAAGC 340
 |||||
 sProLysTyrPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMet 100
 |||||
 CCCCNAATGTTTGTCTTGGTGTGGCAAGTCATAAAGGCTAGACATTGCTATG 400
 |||||
 rAspMetCysProGlyGlyLysArgLysValIleProProSerPheAlaTyrGly 120
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 AGATATGTCCTGGAGAAAGCGAAAGTAGTTATACCCCTTCATTTGCATACGGA 460
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 sGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluLeu 140
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 GGAAAGCTATGCAAGAGGCAAGATTCACCGGATGCTACATTTGATTTTGAATGAA 520
 |||||
 uTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
 |||||
 TTATGCTGTGACCAAGGACACGGAGCATTGAGACATTTAAACAAATAGACATGGAC 580
 |||||
 nAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
 |||||
 TGACAGCGAGCTCTTAAGCCGAGATAAACCTCTACTTGCACAAAGGGAATTTGAAGA 640
 |||||
 pGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePheLysLys 200
 |||||
 TGAAAGCCACGTCGACAAAGTCATATCAGGATGCGAGTTTGTAGAGATATTTTAAAGA 700
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 ATGACCATGATGTGTGATGGCTTCATTTCTCCCAAGATACAAATGTATACCAACAC 760
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 pGluLeu 222
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 TGAACCTA 769

9909 787 bp mRNA linear EST 01-MAY-2003
 COURT_13903492 NIH MGC 147 Homo sapiens cDNA clone
 E:30341652 5', mRNA sequence.
 9909
 9909.1 GI:30284429

sapiens (human)

sapiens
 ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 bases 1 to 787)

MGC <http://mgc.nci.nih.gov/>.
 onal Institutes of Health, Mammalian Gene Collection (MGC)
 blished (1999)

act: Robert Strausberg, Ph.D.

l: cgapbs-remail.nih.gov

ue Procurement: Dr. Stefan Hansson

A Library Preparation: Michael J. Brownstein (NHGRI) with help
 advice from Piero Carninci (RIKEN)

A Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Sequencing by: Agencourt Bioscience Corporation

ae distribution: MGC clone distribution information can be

d through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>
 Plate: NDAM373 row: h column: 13
 High quality sequence stop: 621.

FEATURES

source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /note="organ: placenta; Vector: pBluescriptR;
 all-XhoI; Site 2: BamH; Oligo-dT primed using
 5'-TTTTTATTTTATTTTNN-3', size-selected for a
 insert size 2.3 kb and normalized to 10⁷ 5' th
 primary library enriched for full-length clone
 constructed using the Cap-trapper method (Car
 preparation). Library constructed by M. Brown
 (NIH/NHGRI, National Institutes of Health). N
 a NIH_MGC library."

ORIGIN

Alignment Scores:
 Pred. No.: 3,59e-115 Length: 787
 Score: 1145.00 Matches: 219
 Percent Similarity: 98.65% Conservative: 1
 Best Local Similarity: 98.21% Mismatches: 1
 Query Match: 96.30% Indels: 2
 DB: 14 Gaps: 0

US-10-015-480A-180 (1-222) x CB989909 (1-787)

QY 1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTyr
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 Db 100 ATGCCAAACCATGATTTCTTATTCAGATTCATTTCTTTTATCTGTG
 |||||
 QY 21 PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGln
 |||||
 Db 160 TTTACTGCTCAGACACAAAGAGAGGAGACCCGAAAGAGTGAATAGAG
 |||||
 QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAla
 |||||
 Db 220 CATCGTCCAGAAAACTGCTCTAAGACAAGCAAGAGGAGGAGACCTACTAAATGC
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 QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsr
 |||||
 Db 280 GACGGCTACCTGGCTAAAGACGGCTCGAAATTTCTACTGACGGCGGACACAAAA
 |||||
 QY 81 HisProLysTyrPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIle
 |||||
 Db 340 CACCCCAATGTTTGTCTTGTGTGGCAAGTCATAAAGGCGCTAGACATT
 |||||
 QY 101 ThrAspMetCysProGlyGluLysArgLysValIleProProSerPheAla
 |||||
 Db 400 ACAGATATGTCCCTGGAGAAAGCGAAAGTAGTTATACCCCTTCATTTGCA
 |||||
 QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGlu
 |||||
 Db 460 AAGGAAGGCTATGCAAGAGGCAAGATTTCCACCGGATGCTACATTTGATTGAG
 |||||
 QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAsp
 |||||
 Db 520 CTTTATGCTGTGACCAAGGACCCGAGGAGCATTTGAGACATTTAAACAAATAGAC
 |||||
 QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPhe
 |||||
 Db 580 AATGACAGGCGAGCTCTCTAAAGCGGAGATAAACCTCTACTTGTGCAAGGGAATTT
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 QY 181 AspGluLysProArgAspLysSerTyrGlnAspAlaValLeuGluAspIlePhe
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snAspHisAspGlyAspGlyPheIleSer-ProLysGluTyrAsnValTyr-GlnHisA 220
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dGlu 221
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 TGAA 764

27688 800 bp mRNA linear EST 04-OCT-2001
 074295F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5166166 5',
 A sequence.

27688
 27688.1 GI:15939238

o sapiens (human)
 o sapiens
 ariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 (bases 1 to 800)
 -MGC <http://mgc.nci.nih.gov/>.

ional Institutes of Health, Mammalian Gene Collection (MGC)
 ublished (1999)

tact: Robert Strausberg, Ph.D.

il: cgaps-remail.nih.gov

sue Procurement: Life Technologies, Inc.

NA Library Preparation: Life Technologies, Inc.

NA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

A Sequencing by: Incyte Genomics, Inc.

one distribution: MGC clone distribution information can be

nd through the I.M.A.G.E. Consortium/LLNL at:

p://image.llnl.gov

te: LLAM11412 row: n column: 23

h quality sequence stop: 794.

Location/Qualifiers

1. .800

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

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/tissue_type="medulla"

/lab_host="DH10B"

/clone_lib="NIH_MGC_119"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 site 2: EcoRV (destroyed); RNA source normal medulla from

anonymous male age 27. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.3 kb, insert size range

0.9-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 013. Note:

this is a NIH_MGC Library."

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1121.50 Matches: 220

ity: 98.21% Conservativity: 0

larity: 98.21% Mismatches: 1

94.32% Indels: 4

12 Gaps: 1

180 (1-222) x B1827688 (1-800)

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|||||

hethrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGluValLeu 40

|||||

TTACTGCTCAGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 198

QY 41 HisArgProGluAsnCysSerLysThrSerLysGlyAspLeuLeuAsnA
 |||||
 Db 199 CATCGTCCAGAAACTGCTCTAAGACAAGCAAGAGGAGACCTACTAATG
 QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnA
 |||||
 Db 259 GACGGCTACCTGGCTAAAGACGGCTGAATTTCTACTGCAGCGGACACAAA
 QY 81 HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspI
 |||||
 Db 319 CACCCCAATGGTTGTTCTTGGTGTGGCAAGTCAATAAAGCCCTAGACA
 QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheA
 |||||
 Db 379 ACAGATATGTGCTCGAGAAAAGCGAAAGTAGTTATATACCCCTTCATTG
 QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheG
 |||||
 Db 439 AAGGAAGGCTAT--GAAGCAAGATTCACCGGATGCTACATTGATTTTGF
 QY 141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleA
 |||||
 Db 496 CTTTATGCTGTGACCAAGAGACCCAGGAGCATTGACACATTTAAACAAATAG
 QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluP
 |||||
 Db 556 AATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAGAGGAATT
 QY 181 AspGluLysProArgAspLysSerTyr-GlnAspAlaValLeuGluAspIle
 |||||
 Db 616 GATGAGAGCCAGCGTGACAGTCATATCCAGGATGCAGTTTATAGAGATATT
 QY 200 sAsnAspHisAspGlyAspGlyPheIleSerProLysGluTyr-AsnValTyr
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 Db 676 GAATGACCATGATGTGTGATGGCTTCATTCTCCCAAGGATACAAATGTATAC
 QY 220 spGluLeu 222
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 Db 736 ATGAACATA 743

RESULT 5

BG939266

LOCUS

DEFINITION

clone NTBC_cn31e10 random, mRNA sequence.

ACCESSION

BG939266

VERSION

BG939266.1 GI:14338638

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

AUTHORS

1 (bases 1 to 643)

Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,

Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.I., Yang

Robey,P.G., Hotchkiss,R.N. and Francomano,C.A.

SGAP: The Skeletal Genome Anatomy Project

Unpublished (1997)

Contact: Libin Jia

Medical Genetics Branch

National Human Genome Research Institute

10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267

Tel: 301-402-4877

Fax: 301-496-7157

Email: libin@helix.nih.gov

DNA Sequencing and analyses by National Institutes of H

Intramural Sequencing Center (NISC).

Plate: 31 row: e column: 10

Seq primer: -21M13 forward primer (ABI).

FEATURES

Location/Qualifiers

1..643

/organism="Homo sapiens"

/mol_type="mRNA"

7479
7479.1 GI:31583547

b

[illegible]

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 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
 CTTTATGCTGTGACCAAGAGCAGGAGCATGTGAGACATTTAAACAATAGACATGGAC 571
 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLys 180
 AATGACAGGCAGCTCTTAAGCCGAGATAAACCCTACTTGCRAAGGGAATTTGAATAA 631
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 sAsnAspHisAsp-GlyAsp-GlyPheIleSer-ProLysGluTyrAsn 215
 TATGACCATGATGGGTGATGGGCTTCATTTCTCCCGAGGAATACAAT 740

374396 734 bp mRNA linear EST 20-OCT-2000
 148821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891173 5',
 VA sequence.

374396
 374396.1 GI:10323172

no sapiens (human)
 no sapiens
 karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 amalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 (bases 1 to 734)
 i-MGC <http://mgs.nci.nih.gov/>.
 ional Institutes of Health, Mammalian Gene Collection (MGC)
 ublished (1999)
 tract: Robert Strausberg, Ph.D.
 il: cgapbs-remail.nih.gov
 issue Procurement: DCTD/BTP/Gazdar
 NA Library Preparation: Life Technologies, Inc.
 NA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 A Sequencing by: Inyte Genomics, Inc.
 one distribution: MGC clone distribution information can be
 nd through the I.M.A.G.E. Consortium/LLNL at:
 p://image.llnl.gov
 ite: LAM9675 row: j column: 06
 ph quality sequence stop: 602.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3891173"
 /tissue_type="large cell carcinoma, undifferentiated"
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 /clone_lib="NIH_MGC_69"
 /note="Organ: lung; Vector: pCMV-Sport6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.1 kb. Library constructed by Life
 Technologies."

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 1.88e-100 Length: 734
 1010.50 Matches: 203
 ity: 92.41% Conservative: 4
 larity: 90.62% Mismatches: 11
 84.99% Indels: 6
 10 Gaps: 1

180 (1-222) x BE874396 (1-734)

etProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTrpGlyLeu 20

Db 31 ATGCCAAAACCATGCATTTCTTATCAGATTCATGTTTCTTTATCTGT
 QY 21 PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleG
 Db 91 TTTACTGCTCAGAGACAAAAGAAAGAGAGAGACCCGAGAAGTGAATAAG
 QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnA
 Db 151 CATGCTCCAGAAAACCTGCTCTAAGACAAGCAAGAGAGAGAGACCTACTAAATG
 QY 61 AspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnA
 Db 211 GACGCTACCTGGCTTAAGACGGCTCGAAATTTCTACTGACGCGGACACAAA
 QY 81 HisProLysTrpPheValLeuGlyValGlyGlnValIleLysGlyLeuAspI
 Db 271 CACCCCAATGGTTGTTCTTGGTGGTGGCAAGTCATAAAAGGCGCTAGACA
 QY 101 ThrAspMetCysProGlyGluLysArgLysValValIleProProSerPheA
 Db 331 ACAGATATGTGCCCTGGAGAAAAGCGAAAGTAGTTATACCCCTTCATTG
 QY 121 LysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIle-Phe
 Db 391 AAGGAAGGCTATGACAGAGCAAGATTCACCGGATGCTACATGATTTCTT
 QY 140 uLeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIle
 Db 451 ACTTTATGCTGTGACCAAGAGCAGCAGGATTCAGACATTTAAACAAATA
 QY 160 pAsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGlu
 Db 511 CAATGACAGGCGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAGAGGGA
 QY 180 sAspGluLysProArgAsp-LysSerTyrGlnAspAlaValLeuGluAsp-I
 Db 571 AGATGAGAGCCAGCTGACACAGTCATATCAGGATGAGTTTCACAGACTA
 QY 200 LysAsnAspHis-Asp-GlyAspGlyPhe---IleSerProLysGluTyrAsi
 Db 631 ACCACTGACCATCATCGGAATGCCCTTCATTTCTCCCGAGGATTAACAC
 QY 218 ln 218
 Db 691 AA 692

RESULT 8
 CB570987
 LOCUS
 DEFINITION
 AGENCOURT 12993310 NIH_MGC_165 Mus musculus cDNA clone
 IMAGE:30278220 5', mRNA sequence.

ACCESSION
 VERSION
 CB570987
 CB570987.1 GI:29490517
 EST.

SOURCE
 Mus musculus (house mouse)
 Mus musculus
 Mus musculus

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; M
 1 (bases 1 to 734)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collectic
 Unpublished (1999)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Leslie L. Heckert
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LI
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM32 row: e column: 13

ispMetCysProGlyGluLysValValleProProSerPheAlaTyrGlyLys 121
 :ATATGTCCTGGAGAGAGCGAAAGTGATTATACCCCTCTCTTTCATATGGAAG 398
 :luGlyTyrAlaGluGlyValleProProAspAlaThrLeuLeuPheGluLeu 141
 :AAGCTATGAGAAAGCAAGATTCCACCTAATGCAACATTGATTTTGGAGATTGAACCT 458
 :YrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAspAsn 161
 :ATGCTGTAAACCAAGAGGACCGACGACATTGAACATTTAAACAGATAGACCGACAAT 518
 :aspArgGlnLeuSerLysAlaGluLeuLeuLeuTyrLeuGlnArgGluPheGluLysAsp 181
 :ACAGACAACTCTCTAAACCTGAGATAAATCATTACCTGAAAAAGGAATTTGAAAAAGAT 578
 :luLysProArgAspLysSerTyrGlnAspAlaValleu 194
 :AGAAGCCACGTGACAAATCATATCAGAAATGACGTTTGA 617

51693 602 bp mRNA linear EST 16-SEP-2002
 19C12.y1 McCarrey Eddy type A spermatogonia Mus musculus CDNA
 ne IMAGE:6442846 5' similar to TR:O54998 O54998 FK506-BINDING
 TEIN. ; mRNA sequence.
 51693
 51693.1 GI:22934554

musculus (house mouse)
 musculus
 aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 malia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 (bases 1 to 602)
 arrey,J., Eddy,M., Marra,M., Hillier,L., Clifton,S., Pape,D.,
 tin,J., Wylie,T., Pante,M., Bowers,Y., Theising,B., Gibbons,M.,
 ter,E., Tsagareishvili,R., Ronko,I., Maguire,L., Kennedy,S.,
 nett,J., Waterston,R. and Wilson,R.
 HS Mouse
 ublished (2002)
 tact: McCarrey/Eddy NIEHS Mouse
 HS Mouse
 hington University School of Medicine
 4 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 : 314 286 1800
 : 314 286 1810
 il: est@watson.wustl.edu
 s clone is available royalty-free through LNL ; contact the
 GE Consortium (info@image.llnl.gov) for further information.
 :2067958
 primer: -40RP from Gibco
 h quality sequence stop: 421.
 Location/Qualifiers
 1. .602
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CD-1"
 /db_xref="taxon:10090"
 /clone="IMAGE:6442846"
 /sex="male"
 /tissue_type="type A spermatogonia, pooled from multiple
 mice"

/dev_stage="8 day"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="McCarrey Eddy type A spermatogonia"
 /note="Organ: testis; Vector: pBluescript SK+
 (Stratagene); Site 1: XhoI; Site 2: EcoRI; CDNA oligo
 dt-primed [5'-(GA)10-CTAGTCGAGTTTTTTTTTTT-3'] and
 directionally cloned using 5' linkers 5'-AATTGCGCAGAG-3'
 and 5'-CTGTCGCG-3'. Size selection of >400bp material
 gives average insert size ranging from 1-2 kb. Library was
 mass excised (from lambda-UniZAP-XR) and resulting

single-stranded phagemids were prepped and tr
 into DH10B. Library contains 96.5% recombinan
 References: J. Androl. 20:635-639 and Gene 25
 Library constructed and donated by J. McCarre
 (Southwest Foundation for Biomedical Research
 Genetics); excision done by E.M. Eddy, Ph.D.
 Institutes of Health, National Institute of I
 Health Sciences). Original lambda-based libr
 available through ATCC, catalog #63416."

ORIGIN

Alignment Scores:
 Pred. No.: 1.32e-91 Length: 602
 Score: 929.00 Matches: 175
 Percent Similarity: 91.50% Conservative: 8
 Best Local Similarity: 87.50% Mismatches: 17
 Query Match: 78.13% Indels: 0
 DB: 13 Gaps: 0

US-10-015-480A-180 (1-222) x BU551693 (1-602)

QY 8 LeupheArgPheIleValPhePheTyrLeuTyrGlyLeuPheThrAlaGlnAla
 :|||||
 Db 2 CTATTCAGACTAGCAGTTTCTTAGCCTCTGGTGTGTTCGCGATGCTCAGG
 :|||||
 QY 28 LysGluGluSerThrGluGluValLysIleGluValLeuHisArgProGluAla
 :|||||
 Db 62 AAAGAGAAAGCACTGAGGAAGTGAATAAGAGTTTTCACCGTCCAGAA
 :|||||
 QY 48 LysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyrAspGlyTyrLeuAla
 :|||||
 Db 122 AAAACAAGCAGGAAAGAGAGACTTGTCTAAATGCCCATTTACGATGGCTACTTGG
 :|||||
 QY 68 GlySerLysPheTyrCysSerArgThrGlnAsnGluGlyHisProLysTyrP
 :|||||
 Db 182 GGCTCCCAATTTCTACTGACCGCGACACAGATGAAGGCCACCCCAATGGT
 :|||||
 QY 88 GlyValGlyGlnValIleLysGlyLeuAspIleAlaMetThrAspMetCysP
 :|||||
 Db 242 GGTGTGGACATGTCTATAAGGGGGTGGACATGCTATGATGACATGTGCCC
 :|||||
 QY 108 LysArgLysValValIleProProSerPheAlaTyrGlyLysGluGlyTyrAl
 :|||||
 Db 302 AAGAGAAAGTGATTTATCTCTCTTCATTTGCATATGGAAGAAAGGCTATGC
 :|||||
 QY 128 LysIleProProAspAlaThrIleuIlePheGluIleGluLeuTyrAlaValT
 :|||||
 Db 362 AAGATTCCACCCCAATGCAACTCTGATGTTTGAGATTGAACCTTTATGCTGTGAC
 :|||||
 QY 148 ProArgSerIleGluThrPheLysGlnIleAspMetAspAsnAspArgGlnLe
 :|||||
 Db 422 CCAAGGAGCATTTGAACATTTAAGCAAAATAGACACGATAATGACCGGCACT
 :|||||
 QY 168 AlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLysAspGluLysProAr
 :|||||
 Db 482 GCTGAGATAGAGCTTTACTTTACAGAAGGACTTTGAAAAAGATGCAAAACCCCG
 :|||||
 QY 188 SerTyrGlnAspAlaValLeuGluAspIlePheLysLysAsnAspHisAspGl
 :|||||
 Db 542 TCATATCAGAGCGCAGCTTTTGGAGATATCTTTTAAGAAAAAATGACCAATATG

RESULT 11

EX485892
 LOCUS
 DEFINITION
 DXFP2p686C11249_r1 686 (synonym: hlccc3) Homo sapiens CDN
 DXFP2p686C11249 5', mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Hom

(bases 1 to 602)
 orge W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B.,
 es, H.W., Weil, B., Amid, C., Oeanger, A., Fobo, G., Han, M. and
 mann, S.
 (Ansoerge, W., Krieger, S., Regiert, T., Rittmueller, C., et al.)
 ublished (2003)
 tact: MIPS

S
 Olstaedter Landstr.1, D-85764 Neuherberg, Germany
 s is the 5' sequence of the clone insert
 ne from S. Wiemann, Molecular Genome Analysis, German Cancer
 earch Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 elburg/Germany) within the cDNA sequencing consortium of the
 nan Genome Project.

SI sequence available.

s clone (DKFZp686C11249) is available at the RZPD in Berlin.
 ase contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 lin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers

1..602
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp686C11249"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="686 (synonym: hlcc3)"
 /note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
 cDNA-collection"

1: 2.66e-89 Length: 602
 908.00 Matches: 171
 ty: 96.61% Conservative: 0
 arity: 96.61% Mismatches: 6
 76.37% Indels: 0
 13 Gaps: 0

80 (1-222) x BX485892 (1-602)

tProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTrpGlyLeu 20
 GCCAAACCATCATCTTATTCAGATTCATGTTTCTTTTATCTGTGGGCGCTT 129
 eThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGluValLeu 40
 TACTGCTCANAGACAAAGAGAGAGAGACCCGGAANTGAAATAGAAATTTTG 189
 sArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuAsnAlaHisTyr 60
 TCGTCAGAAAACCTGCTCTAAGACAAGCAAGAGGAGACCTACTAAATGCCATAT 249
 pGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGly 80
 CGGTACTCTGGCTTAAGACGGCTCGAAATTTCTACTGCAGCCGACACAAATGAAGGC 309
 sProLysThrPheValLeuGlyValGlyGlnValIleLysGlyLeuAspIleAlaMet 100
 CCCCAAATGTTAGTCTTGTGTGTGGCAAGTCATAAAGGCCGTAGCATTTGCTATG 369
 rAspMetCysProGlyGluLysArgLysValValIleProProSerPheAlaTyrGly 120
 AGATATGTCCTCGAGAAAAGCGAAAGTAGTTATACCCCTTCATTTGCATACGGA 429
 sGluGlyTyrAlaGluGlyIleProProAspAlaThrLeuIlePheGluIleGlu 140
 GGAAGCTATGCAAGGCAAGATTCACCGGATGCTACATTCATTTTTCAGATTAA 489
 uTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAsp 160
 TTATGCTGTACCAAGNCCAGGACATTGAGACATTTAAACAAATAGACATGGAC 549

QY 161 AsnAspArgGlnLeuSerLysAlaGluIleAsnLeuTyrLeuGlnArgGlu
 Db 550 ATGACAGGCGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAGAGGAA

RESULT 12

CB959508

LOCUS

DEFINITION

AGENCOURT 13887721 NIH_MGC_147 Homo sapiens cDNA clone

IMAGE:30341701 5', mRNA sequence.

ACCESSION

CB959508

VERSION

CB959508.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho

1 (bases 1 to 800)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collectio

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgsbbs@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

cDNA Library Preparation: Michael J. Brownstein (NHGRI

and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LL

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM373 row: j column: 14

High quality sequence stop: 469.

Location/Qualifiers

1..800

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30341701"

/tissue_type="Human Placenta"

/lab_host="DH10B Tona"

/clone_lib="NIH MGC 147"

/note="Organ: placenta; Vector: pBluescriptR; ;

all-XhoI; Site_2: BamH; Oligo-primed using 1

5'-TTTTTTTTTTTTTT-3', size-selected for a

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primary library enriched for full-length clones

constructed using the Cap-trapper method (Carl

preparation). Library constructed by M. Brown

(NIH/NHGRI, National Institutes of Health). NC

a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.: 2.97e-87 Length: 800

Score: 890.50 Matches: 180

Percent Similarity: 90.78% Conservative: 7

Best Local Similarity: 87.38% Mismatches: 12

Query Match: 74.89% Indels: 7

DB: 14 Gaps: 2

US-10-015-480A-180 (1-222) x CB959508 (1-800)

QY 1 MetProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTrp

Db 100 ATGCCAAAACCATGATTTCTTATTCAGATTCATTTCTTTTATCTGTGG

QY 21 PheThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGlu

Db 160 TTTACTGCTCAGAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG

QY 41 HisArgProGluAsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAla

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TATCGTCAGAAACTGCTCTAAGACAGCAAGCAAGAGGAGACCTACTAAATGCCCATTTAT 279
aspGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80
HACGGCTACCTGGCTTAAAGACGGCTCGAAATCTACTGACGGGACACAAAATGAAGGC 339
HisProLysTrpPheValLeuGlyValGlyGlnValLleLysGlyLeuAspIleAlaMet 100
ACCCCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 399
ThrAspMetCysProGlyGluLysArgLysValLleProProSerPheAlaTyrGly 120
CAGTATGTCCTCGGAAAGCAAGAAAGTAGTTATACCCCTTATTTCATACGGA 459
ysGluGlyTyrAlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGlu 140
AGGAAGCTATGTCAGAAAGCAAGATCCCGCATGCTACATTGATTTTGATTTGAATGAA 519
euTyrAlaValThrLysGlyProArgSerTleGluThrPheLysGlnIleAspMetAsp 160
TTTATGCTGTGACCAAGGACCAAGCAAGCAATTCAGACATTTAAACAAATAGACTGGAC 579
snAspArgGlnLeuSerLysAla--GluIleAsnLeu-Tyr-LeuGlnArgGluPhe-- 178
ATGACAGGAGCTCTTCTTAAGCCCGCAATTAACCTCTTCTTGTGAAAGGGAATTTTG 639
GluLysAspGluLysProArgSerLysSerTyrGlnAspAlaValLeuGluAspIlePh 198
AAAAAATGAGAAACCCACCTTGACAAAGTCCATATTTCAGGATG-----CAGGTTTT 693
LysLysAsn 201
:|||||
AGAAAAAT 703

64616      604 bp      mRNA      linear      EST 12-MAR-2002
Og11.y1 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus
culus cDNA clone IMAGE:5665748 5' similar to TR:054998 O54998
06-BINDING PROTEIN. ;, mRNA sequence.
64616
64616.1 GI:16339021
musculus (house mouse)
musculus
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 604)
ton.D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
ishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
lier,I., Marra,M., Pape,D., Wyllie,T., Martin,J., Blustain,A.,
natt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
enas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
liams,T., Jackson,Y. and Bowers,Y.
ocrine Pancreas Consortium
ublished (2000)
ar_ESTs: id40g11.xl
act: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
ocrine Pancreas Consortium
ard University, Howard Hughes Medical Institute
: of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
02138
: 617-495-1812
: 617-495-8557
il: dmelton@biohp.harvard.edu
rary was constructed by Dr. Douglas Melton DNA sequencing by:
ingron University Genome Sequencing Center For information on
ining a clone please contact: Juliana Brown
wnefas.harvard.edu)
:1952074 This sequence now available from the IMAGE consortium,
clone orders contact: info@image.llnl.gov
1 quality sequence stop: 427.
Location/Qualifiers

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source

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/mol_type="mRNA"
/strain="ICR"
/db_xref="taxon:10090"
/clone="IMAGE:5665748"
/sex="Both for embryonic & newborn, male for :
adult islet"
/dev_stage="Embryonic day 10.5, E12.5, E16.5,
adult, mixed"
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/clone_lib="Melton Normalized Mixed Mouse Pan
N1-MMS1"
/notes="Vector: pSPORT1; Site 1: Not I; Site 2:
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pancreas, newborn pancreas, adult pancreas, i
islets of Langerhans were separately construc
SuperScript plasmid library kit (Life Techno
was made by oligo-dT priming and size-selectec
fractionation. Libraries were amplified once c
support and plasmid DNA from each library was
and mixed in equal amounts. The mixed library
normalized by method #4 from Bonaldo, Lennon,
1996 Genome Research 6:791-806; 0.5 microgram
single-stranded mixed library plasmid DNA was
5 micrograms PCR product representing mixed li
inserts and hybridized to an EcoT of 6. Singl
(unhybridized) plasmids were isolated by hydr
chromatography and used to make this library.

```

ORIGIN

```

Alignment Scores:
Pred. No.: 1 39e-84      Length: 604
Score: 865.00      Matches: 164
Percent Similarity: 90.53%      Conservative: 8
Best Local Similarity: 86.32%      Mismatches: 18
Query Match: 72.75%      Indels: 0
DB: 12      Gaps: 0

US-10-015-480A-180 (1-222) x BI964616 (1-604)

QY 5 MetHisPheLeuPheArgPheIleValPhePheTyrLeuTyrGlyLeuPheTh
Db :|||:|
35 ATGAATCTCTTATCAGACTAGCAGTTTCTTAGCTGTGGTGTGTTCGGA
QY 25 ArgGlnLysGlyGluSerThrGluGluValLysIleGluValLeuHisAr
Db :|||:|
95 GGACAAACAAAAAGAAAGACACTGAGGAAGTGAAATAGAAAGTTTGCACCG
QY 45 AsnCysSerLysThrSerLysLysGlyAspLeuLeuAsnAlaHisTyrAspGI
Db :|||:|
155 AACTGCTCCAAACCAAGCAGGAAAGAGACTTGTAAATGCCCATTTACATGG
QY 65 AlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGlyHisPr
Db :|||:|
215 GCTAAAGACGGCTCCAAATTTCTACTGACGCGGACACAGATGAAGGCCACCC
QY 85 PheValLeuGlyValGlyGlnValLleLysGlyLeuAspIleAlaMetThrAsi
Db :|||:|
275 TTGTGTTCTGTGTGTCGACATGTCTATAAAGGGGCTGGACATTCGTATGATGA
QY 105 ProGlyGluLysArgLysValValIleProProSerPheAlaTyrGlyLysGln
Db :|||:|
335 CCTGGGGAAAGAGAAAGTGATATACCTCTCTTCAATTGCATATGGAAGAAG
QY 125 AlaGluGlyLysIleProProAspAlaThrLeuIlePheGluIleGluLeuTy
Db :|||:|
395 GCAGAAGGCAAGATTCCACCCCAATGCAACTCTGTATGTTTGTGATTTGAATTTA
QY 145 ThrLysGlyProArgSerIleGluThrPheLysGlnIleAspMetAspAsnAsi
Db :|||:|
455 ACCAAAGGACCAAGGAGCAATTGAACACATTTAAGCAATAGACACGGAATATGA

```

```

euSerLysAlaGluIleAsnLeuTyrLeuGlnArgGluPheGluLysAspGluLysPro 184
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
TCTCCAAAGCTGAGTAGAGCTTTACTTACAGAGGAGCTTTGAAAAAGATGCAAGCC 574

rGAspLysSerTyrGlnAspAlaValLeu 194
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GTGACAAAGTCATATCAGAGGAGGAGTITTTG 604

96952 644 bp mRNA linear EST 06-NOV-2001
59-1-C9.R HOA (Human Osteoarthritic Cartilage) Homo sapiens
A, mRNA sequence.
96952
96952.1 GI:14307193
; sapiens (human)
; sapiens
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
nalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 644)
r,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mac,J.,
e,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
t,M.W.
itification and initial characterization of 5000 expressed
enced tags (ESTs) each from adult human normal and
oarthritic cartilage cDNA libraries
oathr. Cartil. 9 (7), 641-653 (2001)
12651
17177
act: Sanjay Kumar
09
oSmithKline
Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
610-270-7245
610-270-5598
l: sanjay.kumar-1@gsk.com
primer: 77
Location/Qualifiers
1. .644
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/note="vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"

: 1.44e-83 Length: 644
856.00 Matches: 164
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arity: 98.80% Mismatches: 2
71.99% Indels: 1
12 Gaps: 0

30 (1-222) x BG96952 (1-644)
-ProLysThrMetHisPheLeuPheArgPheIleValPhePheTyrLeuTyrGlyLeu 20
3CCAAAAACCATGCTTTCTTATCAGATTCAATGTTTCTTTTATCTGTGGGCGCTT 203
rThrAlaGlnArgGlnLysLysGluGluSerThrGluGluValLysIleGluValLeu 40
TACTGCTCAGAGACAAAAGAGAGAGAGAGACCGAAGAGTGAAGATTTTGT 263
rArgProGluAsnCysSerLysThrSerLysGlyAspLeuLeuAsnAlaHisTyr 60
TCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAGAGAGAGAGAGAGAGAGAGAT 323
rGlyTyrLeuAlaLysAspGlySerLysPheTyrCysSerArgThrGlnAsnGluGly 80

```

```

Db 324 GACGGCTACTGCTAAGACGCTCGAATTCCTCTGACGCGGACACAAA
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
81 HisProLysTrpPheValLeuGlyValGlnValIleLysGlyLeuAspI
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
384 CACCCCAAAATGTTTCTTCTTGTGTTGGCAAGTCATAAAGGCTAGACA
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 ThrAspMetCysProGlyLysArgLysValValIleProSerPheAl
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
444 ACAGATATGTCCTCGAGAAAAGCGAAAGTAGTTATACCCCTTCATTTC
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 LysGluGlyTyrAlaGluGlyLysIleProAspAlaThrLeuIlePheG
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
504 AAGGAAGGCTATGCAGAGGCGAGATCCCGGATGCTACATGATTTTGA
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
141 LeuTyrAlaValThrLysGlyProArgSerIleGluThrPheLysGlnIleAs
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
564 CTTTATGCTGTGAC-AAAGGACACGCGGCGCATTGAGACATTTAAACAATAGA
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
161 AsnAspArgGlnLeuSer 166
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
623 AATGACAGCGCTCTCT 640

RESULT 15
Al182368/c
LOCUS
DEFINITION
673 bp mRNA linear EST
ud59f01.x1 Sugano mouse liver mlia Mus musculus cDNA cl
IMAGE:1451065 3' similar to SW:FKB2_MOUSE P45878 FK506-
PROTEIN PRECURSOR ;, mRNA sequence.
Al182368
Al182368.1 GI:3733006
EST.
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu
1 (bases 1 to 673)
Maiba, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. &
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; cont
IMAGE Consortium (info@image.llnl.gov) for further infor
MG1:924391
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 467.
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Location/Qualifiers
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[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cdi
ligated to a DraIII adaptor [TGTGGCCTACTGG], (

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and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTCTCTCTAAAGCTGCG and 3' end primer CGACCTGAGCTGAGCACA."

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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April 9, 2004, 10:40:36 ; Search time 86 Seconds
(without alignments)

1432.548 Million cell updates/sec

US-10-015-480A-180

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

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ter than or equal to the score of the result being printed,
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ALIGNMENTS

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; Sequence 33, Application US/09205258

; Patent No. 6525174

; GENERAL INFORMATION:

; APPLICANT: Young et al.

; TITLE OF INVENTION: 207 Human Secreted Proteins

; FILE REFERENCE: P2007P1

; CURRENT APPLICATION NUMBER: US/09/205,258

; EARLIER FILING DATE: 1998-12-04

; EARLIER APPLICATION NUMBER: PCT/US98/11422

; EARLIER FILING DATE: 1998-06-04

; EARLIER APPLICATION NUMBER: 60/048,885

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,375

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,881

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,880

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,896

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,020

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,876

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,895

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,884

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,894

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,971

; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/048,964

; EARLIER FILING DATE: 1997-06-06

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mo sapiens

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57)

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64)

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; Patent NO. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; CURRENT FILING DATE: 1998-12-04
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06

